

PA (STER-) STERREBELD BIOTECHNOLOGIE NORTH AMERICA.
 XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
 XX WPI: 2000-376485/32.
 XX Novel methods for purifying recombinant human erythropoietin from
 PT mammalian cell culture reagents -
 XX Claim 16; Page 18; 30pp; English.
 XX The present invention relates to a method for purifying erythropoietin
 CC (EPO) for treatment of disease, especially anaemia. The method involves
 CC treating cell culture supernatants with differential precipitation,
 CC hydrophobic interaction chromatography, diafiltration, anionic and
 CC cationic exchange chromatography and molecular exclusion
 CC chromatography. The present sequence is the protein from the culture
 CC supernatant of transfected cell lines, after purification by the above
 CC process. The sequence shows total homology with natural human EPO.
 CC The advantage of this method is that high purity and quality EPO is
 CC produced. A further advantage is that the process does not involve the
 CC use of organic solvents that may harm the environment.
 XX SQ Sequence 165 AA;
 Query Match 100.0%; Score 846; DB 21; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYANKRMEVGQQA 60
 DB 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYANKRMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 QY 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
 DB 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
 RESULT 2
 ID AAB03760
 XX AAB03760 standard; protein; 165 AA.
 AC AAB03760;
 XX 04-OCT-2000 (first entry)
 XX Human erythropoietin (EPO) amino acid sequence.
 XX Erythropoietin; EPO; human; erythroblast differentiation; anaemia;
 KW large scale production; renal failure.
 XX Homo sapiens.
 XX WO200027997-A1.
 XX 18-MAY-2000.
 XX 08-NOV-1999; 99WO-US26240.
 XX 06-NOV-1998; 98AR-0105611.
 XX 23-FEB-1999; 99AR-0100681.
 XX (STER-) STERREBELD BIOTECHNOLOGIE NORTH AMERICA.
 XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;
 XX WPI: 2000-376519/32.
 XX A novel method for the massive culture of recombinant mammalian cells
 PT

PT producing recombinant human erythropoietin -
 XX Example 8; Page 11-12; 23pp; English.
 XX This sequence represents the human erythropoietin amino acid sequence.
 CC Erythropoietin is a glycoprotein that stimulates erythroblast
 CC differentiation in the bone marrow. The present invention relates to a
 CC method for the large scale production of human EPO from recombinant
 CC mammalian cells. The method comprises culturing mammalian cells which
 CC express recombinant human EPO in culture medium comprising insulin.
 CC Erythropoietin can be used to treat anaemia derived from renal failure.
 CC The method allows for the industrial scale production of EPO, and
 CC overcomes the problems of low reproducibility and output quality which
 XX are encountered with previous production methods.
 SQ Sequence 165 AA;
 Query Match 100.0%; Score 846; DB 21; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYANKRMEVGQQA 60
 DB 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSLNENITVPDTKVNFKYANKRMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
 QY 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
 DB 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
 RESULT 3
 ID AAY99705
 XX AAY99705 standard; protein; 165 AA.
 AC AAY99705;
 XX 15-SEP-2000 (first entry)
 XX Non-glycosylated erythropoietin analogue NGE-166delta.
 XX Human; non-glycosylated erythropoietin analogue; NGEA; haematocrit;
 KW antianaemic; anaemia; erythropoiesis promoter; mutant; mutein.
 XX Homo sapiens.
 XX Synthetic.
 XX WO200032772-A2.
 XX 08-JUN-2000.
 XX 23-NOV-1999; 99WO-US27801.
 XX 30-NOV-1998; 98US-0110289.
 XX (ELIL) LILLY & CO ELI.
 XX Beals JM, Glaesner W, Micanovic R, Millican RL, Witcher DR;
 XX WPI: 2000-412320/35.
 XX N-PSDB; AAA48373.
 XX Non-glycosylated erythropoietic compound useful for increasing
 PT hematocrit level in mammal with insufficient hematocrit levels in
 PT conditions such as anemia, comprises protein covalently bonded to
 PT polymer.
 XX Claim 2; Page 93-94; 94pp; English.
 XX The present sequence is a non-glycosylated erythropoietin analogue
 CC

CC (NGEA) designated NGE-166delta. The protein sequence is identical to
 CC the sequence of wild-type human non-glycosylated erythropoietin NGE
 CC except that Arg at position 166 is deleted. NGE promotes erythropoiesis
 CC and can therefore be used to increase haematocrit levels in mammals
 CC with conditions such as anaemia, in which levels of haematocrit are
 CC insufficient. NGE analogues can also be used to treat such conditions.
 CC NGEAs do not themselves cause a significant increase in haematocrit but
 CC they acquire that property once they are derivatised with polyethylene
 CC glycol polymers. The analogues can be produced using a linkerless
 CC aldehyde modification process. They show stability and bioactivity in
 CC vivo. The nucleotide sequence encoding this protein was constructed
 CC synthetically by in vitro hybridisation using a set of six overlapping
 CC oligonucleotides from the positive strand of human erythropoietin cDNA
 CC with six complementary oligonucleotides (negative strand). The codon
 CC usage was 100% optimised for E. coli codon usage. The hybridised
 CC oligonucleotides were ligated with T4 DNA ligase and the ligation product
 CC amplified by PCR. The nucleotide sequence was used to express the protein
 CC in host cells.

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 21; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
 DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAKAVSGRLSRTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAKAVSGRLSRTLLRALGAQKEAIS 120
 QY 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165
 DB 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165

RESULT 4
 AAY93445

ID AAY93445 standard; protein; 165 AA.

XX AAY93445;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of human erythropoietin.

KW Human; erythropoietin; EPO; anaemia; renal failure.

XX Homo sapiens.

OS WO200028066-A1.

PN 18-MAY-2000.

XX 08-NOV-1999; 99WO-US26238.

XX 06-NOV-1998; 98AR-0105609.

PR 23-FEB-1999; 99AR-0100679.

XX (STER-) STERRENBELD BIOTECHNOLOGIE NORTH AMERICA.

XX Carcagno CM, Criscuolo M, Melo C, Vidal JA;

XX WPI; 2000-376574/32.

XX New host cell producing recombinant human erythropoietin (EPO) used for
 PT large scale production of EPO

PS Claim 1; Page 26-27; 51pp; English.

XX The present sequence represents human erythropoietin protein. The

CC specification describes a host cell line which is used to produce
 CC human erythropoietin (EPO). EPO is a glycoprotein. The cell line
 CC is used for the production of recombinant human erythropoietin. The
 CC protein is used for the treatment of anaemia, especially anaemia derived
 CC from renal failure.

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 21; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60
 DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAKAVSGRLSRTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQWPPEQLQHVDAKAVSGRLSRTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165
 DB 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165

RESULT 5

AAB84525

ID AAB84525 standard; protein; 165 AA.

XX AAB84525;

XX 05-SEP-2001 (first entry)

XX Amino acid sequence of human erythropoietin (EPO) protein.

XX Erythropoietin; EPO; erythropoietin stimulating protein; NESP;
 KW sustained release.

XX Homo sapiens.

XX WO200130320-A1.

XX 03-MAY-2001.

XX 23-OCT-2000; 2000WO-US29257.

XX 22-OCT-1999; 99US-0426566.

PR 13-OCT-2000; 2000US-2222222.

XX (AMGE-) AMGEN INC.

XX Burke P, Klumb L, Murphy K, Herberger J, French DL;

XX WPI; 2001-417552/44.

XX Sustained release composition comprises an active biological
 PT ingredient, notably a protein or other biopolymer, particularly
 PT erythropoietin stimulating protein, in biocompatible, biodegradable
 PT polymeric microparticles

PS Disclosure; Page 56; 61pp; English.

XX The present sequence encodes a human erythropoietin (EPO) protein.

CC The specification describes a composition for the sustained release of
 CC biologically active EPO stimulating protein (NESP). The reduced
 CC frequency of administration of NESP, which requires preferably injection
 CC by skilled personnel, improves patient compliance. Also, sustained
 CC release reduces the nature and severity of any side effects of the drug.

XX SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 22; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSSLNENITVPDVKVNFYAKRMVEVGOQA 60
 DB 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSSLNENITVPDVKVNFYAKRMVEVGOQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
 DB 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
 DB 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165

RESULT 6
 AAB66697
 ID AAB66697 standard; protein; 165 AA.
 XX
 AC AAB66697;
 XX
 DT 06-APR-2001 (first entry)
 XX
 DE Human erythropoietin protein #1.
 XX
 KW Erythropoietin; EPO; reticulocytes; red blood cell;
 KW ethylene glycol; chronic renal failure; AIDS; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200102017-A2.
 XX
 PD 11-JAN-2001.
 XX
 PF 28-JUN-2000; 2000WO-EP06009.
 XX
 PR 02-JUL-1999; 99US-0142243.
 PR 05-AUG-1999; 99US-0147452.
 PR 30-AUG-1999; 99US-0151454.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Burg J, Hilger B, Josel H;
 XX WPI; 2001-147051/15.
 DR
 XX
 PT Novel erythropoietin-glycoprotein conjugate useful for treating
 PT diseases correlated with anemia in chronic renal failure patients, AIDS
 PT and for treating cancer, is linked to polyethylene glycol through
 PT linker -
 XX
 PS Claim 19; Fig 1; 40pp; English.
 XX
 CC The present invention relates to a conjugate comprising, human
 CC erythropoietin glycoprotein (EPO) having at least one free
 CC amino group and having in vivo biological activity of causing
 CC an increase the production of reticulocytes and red blood cells,
 CC covalently linked to 1-3 lower-alkoxy poly(ethylene glycol) groups
 CC through a linker. The invention is useful for preparation of
 CC medicaments for the treatment of prophylaxis of disease correlated
 CC with anemia in chronic renal failure patients (CRF), AIDS and for
 CC the treatment of cancer patients undergoing chemotherapy.
 XX
 SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 22; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSSLNENITVPDVKVNFYAKRMVEVGOQA 60
 DB 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSSLNENITVPDVKVNFYAKRMVEVGOQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
 DB 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165

RESULT 7
 ABB77896
 ID ABB77896 standard; protein; 165 AA.
 XX
 AC ABB77896;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Amino acid sequence of a human erythropoietin (EPO).
 XX
 KW Human; erythropoietin; EPO; glycoprotein; reticulocyte production;
 KW red blood cell production; anaemia; chronic renal failure;
 KW acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
 KW committed erythroid progenitor.
 XX
 OS Homo sapiens.
 XX
 PN WO200249673-A2.
 XX
 PD 27-JUN-2002.
 XX
 PF 08-DEC-2001; 2001WO-EPI4434.
 XX
 PR 20-DEC-2000; 2000EP-0127891.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Burg J, Engel A, Franze R, Hilger B, Schurig HE, Tischer W;
 PI Wozny M;
 XX WPI; 2002-565640/60.
 DR
 XX
 PT Novel conjugate of erythropoietin glycoprotein with polyethylene
 PT glycol, useful for treating diseases correlated with anaemia in chronic
 PT renal failure patients and acquired immunodeficiency syndrome -
 XX
 PS Claim 26; Fig 1; 40pp; English.
 XX
 CC The present sequence represents a human erythropoietin (EPO) protein.
 CC It was used to produce conjugates of the invention. The specification
 CC describes a conjugate comprising an EPO glycoprotein having an N-terminal
 CC alpha-amino group, chosen from human EPO (hEPO) or its analogues (where
 CC hEPO is modified by addition of 1-6 glycosylation sites or a
 CC rearrangement of a glycosylation site). The glycoprotein is covalently
 CC linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo
 CC biological activity of causing bone marrow cells to increase production
 CC of reticulocytes and red blood cells. The conjugate increased circulating
 CC half-life and plasma residence time, decreased clearance, increased
 CC clinical activity in vivo, improved potency and stability, when compared
 CC to unmodified EPO. The EPO conjugate is useful for preparing medicaments
 CC for the treatment and prophylaxis of diseases correlated with anaemia in
 CC chronic renal failure patients (CRF), acquired immunodeficiency syndrome
 CC (AIDS) and for treating cancer patients undergoing chemotherapy. It is
 CC also useful for treating patients by stimulating the division and
 CC differentiation of committed erythroid progenitors in the bone marrow.
 XX
 SQ Sequence 165 AA;

Query Match 100.0%; Score 846; DB 23; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSSLNENITVPDVKVNFYAKRMVEVGOQA 60
 DB 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCSSLNENITVPDVKVNFYAKRMVEVGOQA 60

Db 1 APPRLICDSRVLYRLLEAKEAENITTCACAEHCSLNENITVPDTKVNFYAWKRMVEVQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSLTLTLLRALGAQKEAIS 120
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSLTLTLLRALGAQKEAIS 120
 QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLLKLYTGEACRTGD 165
 Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLLKLYTGEACRTGD 165

RESULT 8
 AAM53061
 ID AAM53061 standard; protein: 165 AA.
 XX
 AC AAM53061;
 XX
 DT 25-MAR-2002 (first entry)
 XX
 DE Human erythropoietin (hEPO), 165 residue form.
 XX
 KW Human; erythropoietin; EPO; hEPO; haemostatic; red blood cell;
 KW blood disorder; anaemia; chronic renal failure; CRF; AIDS;
 KW acquired immunodeficiency syndrome; cancer chemotherapy; haemostatic;
 KW anti-HIV; antianaemic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 7..161
 FT Modified-site 24
 FT /note= "N-glycosylated"
 FT Disulfide-bond 29..33
 FT Modified-site 38
 FT /note= "N-glycosylated"
 FT Modified-site 83
 FT /note= "N-glycosylated"
 FT Modified-site 126
 FT /note= "O-glycosylated"
 XX
 PN WO200187329-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 08-MAY-2001; 2001WO-EP05187.
 XX
 PR 15-MAY-2000; 2000EP-0110355.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Papadimitriou A;
 XX
 DR WPI; 2002-082943/11.
 XX
 DT Composition useful in the treatment of e.g. AIDS comprises an
 PT erythropoietin protein, and a multiple charged inorganic anion in a
 PT buffer
 XX
 PS Claim 28; Fig 1; 64pp; English.
 XX
 CC The invention relates to liquid pharmaceutical compositions comprising
 CC an erythropoietin (EPO) protein, a multiple negatively charged inorganic
 CC anion in a buffer which maintains the pH of the solution from 5.5-7.0,
 CC and optionally at least one excipient. The erythropoietin used in the
 CC composition is preferably human (AAM53061 or AAM53062) a human
 CC erythropoietin variant containing additional glycosylation sites
 CC (AAM53064-AAM53107), or an erythropoietin with the C-terminal addition
 CC of a C-terminal fragment of human chorionic gonadotropin (AAM53063).
 CC Erythropoietin is a glycoprotein essential for the formation of red blood
 CC cells and is therefore useful in the treatment of blood disorders
 CC characterised by low or defective red blood cell production. The
 CC compositions of the invention can be used in the treatment and prevention
 CC of anaemia in chronic renal failure patients (CRF), AIDS (acquired

CC immunodeficiency syndrome), and/or for the treatment of cancer patients
 CC undergoing chemotherapy. Unlike prior art erythropoietin compositions,
 CC the compositions of the invention do not contain human serum albumin
 CC (thereby avoiding the possibility of viral infections and allergic
 CC reactions associated with this component), are liquid rather than
 CC lyophilisates (and therefore do not need to be reconstituted before
 CC administration), and are stable at elevated temperatures such as 25
 CC degrees Celsius and even 40 degrees Celsius, and therefore can be stored
 CC without refrigeration for prolonged periods without degradation and loss
 CC of activity. The present sequence represents the 165 residue form
 CC of human erythropoietin which is specifically claimed for use in a
 CC composition of the invention.
 XX
 SQ Sequence 165 AA;
 Query Match 100.0%; Score 846; DB 23; Length 165;
 Best Local Similarity 100.0%; Pred No. 1,1e-86;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCACAEHCSLNENITVPDTKVNFYAWKRMVEVQQA 60
 Db 1 APPRLICDSRVLYRLLEAKEAENITTCACAEHCSLNENITVPDTKVNFYAWKRMVEVQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSLTLTLLRALGAQKEAIS 120
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGLSLTLTLLRALGAQKEAIS 120
 QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLLKLYTGEACRTGD 165
 Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLLKLYTGEACRTGD 165

RESULT 9
 AAP70398
 ID AAP70398 standard; protein: 166 AA.
 XX
 AC AAP70398;
 XX
 DT 19-FEB-1991 (first entry)
 XX
 DE Sequence of human erythropoietin (EPO).
 XX
 KW Mega-karyocyte-platelet growth factor; hormone;
 KW mega-karyocyte colony stimulating factor; therapy;
 KW small acetyl cholinesterase positive cell;
 KW erythrocyte growth effect.
 XX
 OS Homo sapiens.
 XX
 PN JP62149624-A.
 XX
 PD 03-JUL-1987.
 XX
 PF 15-AUG-1986; 86JP-0191542.
 XX
 PR 13-SEP-1985; 85JP-0203049.
 PR 15-AUG-1986; 86JP-0191542.
 XX
 PA (KAWA/) KAWAKITA M.
 XX
 DR WPI; 1987-224837/32.
 XX
 PT Megakaryocyte-platelet growth factor - contains as active
 PT component human erythropoietin and is used to treat diseases
 PT caused by decrease in platelets
 XX
 PS Disclosure; Page 181; 8pp; Japanese.
 XX
 CC All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-
 CC platelet growth factor contains human EPO as an active principle.
 CC Human EPO has a megakaryocyte colony-stimulating activity and
 CC increases the ratio of small acetyl cholinesterase positive cell
 CC (SACHB+) which is immature megakaryocyte. Human EPO effects

CC megakaryocyte-platelet system other than an erythrocyte growth
CC effect. Megakaryocyte-platelet growth is usable as a remedy for
CC diseases caused by a platelet decrease.

Seq	Sequence	166 AA;
	Query Match 100.0%; Score 846; DB 8; Length 166; Best Local Similarity 100.0%; Pred. No. 1.1e-86; Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 APPRLICDSRVLYRLLLEAEAEENITTCGAHCSSLNENITVPDTKVNFYAMKRMEVGQQA 60 	
Db	1 APPRLICDSRVLYRLLLEAEAEENITTCGAHCSSLNENITVPDTKVNFYAMKRMEVGQQA 60 	
QY	61 VEVWQGLALLSEAVLRQALLVNSQWPPEQLQHVDPKAVSGURSLTTLRLALGAQKEAIS 120 	
Db	61 VEVWQGLALLSEAVLRQALLVNSQWPPEQLQHVDPKAVSGURSLTTLRLALGAQKEAIS 120 	
QY	121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLUKLYTGCACTGD 165 	
Db	121 PPDAASAAPLRTITADTFRKLFRVYSNFRGKLUKLYTGCACTGD 165 	

RESULT 10
AAR23593
ID AAR23593 standard: Protein: 166 AA.

XX	AAR23593;
XX	AC
XX	DT
XX	20-OCT-1992 (first entry)
DE	Recombinant hematopoietic molecule portion 2.

SO
YY
Homo sapiens.

XX PN W09206116-A.

XX
PF 26-SEP-1991; 91WO-US07053.

AX
PR 28-SEP-1990; 90US-0589958.

XX
PA (ORTH) ORTHO PHARM CORP.XX
PI
Rosen JI:

XX WPI: 1992-150819/18.

Recombinant haematopoietic molecules useful in treating anaemia(s) - comprise IL-3 or GM-CSF, EPO, G-CSF, IL-5 or M-CSF and has early and later myeloid differentiation activity

PS Disclosure; Page 32; 82pp; English.

This protein sequence given comprises the entire amino acid sequence of human erythropoietin (EPO). EPO leads to the maturation of erythrocytes and is therefore designated as a late myeloid differentiation factor (MDF). Within the scope of the invention hybrid molecules were produced which contain at least a portion of an early MDF and at least a portion of a late MDF covalently linked. The EPO sequence given is effective within the scope of the invention in full or in a truncated version. Amino acids 7-161 act as a late MDF when recombined with an early MDF eg. IL-3. These compounds can be used to promote hematopoiesis in a patient. The bonding of the early and late factors allows a very high conc. of late MDF at the surface of a cell which the early MDF is bound. It also allows the early MDA to act more specifically to stimulate only the desired lineage, thus reducing undesirable effects. These compounds are useful for treating anaemias of various origins eg. renal failure and AIDS. It is easier to produce and administer one

CC recombinant molecule rather than two separate molecules.

```

SQ      Sequence    166 AA;

Query Match          100.0%;   Score 846;   DB 13;   Length 166;
Best Local Similarity 100.0%;   Pred. NO. 1.1e-86;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


Qy      1  APPRCDISRVLRYLLLEAKEAENITTCGAEHCSLNENITVPDTKVFNYANKRMVEVGQA 60
|||||
Db      1  APPRCDISRVLRYLLLEAKEAENITTCGAEHCSLNENITVPDTKVFNYANKRMVEVGQA 60
|||||

Qy      61  VEVWOGALLSEAVLRGQALLVNSQSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQKEAIS 120
|||||
Db      61  VEVWOGALLSEAVLRGQALLVNSQSQPWEPLQLHVDKAVSGLSRLTTLRALGAKQKEAIS 120
|||||

Qy      121  PPDASAAPLRTITADTFRKLFVRYSNFLRGKLKLVGTGACRTGD 165
|||||
Db      121  PPDASAAPLRTITADTFRKLFVRYSNFLRGKLKLVGTGACRTGD 165
|||||
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RESULT 11

AAW77780
ID AAW77780 standard; Protein; 166 AA.

AA AAW77780:

XX	
DT	24-NOV-1998 (first entry)
XX	
DE	Human EPO receptor agonist polypeptide.

Haematopoietic

KW dendritic cell.
KW infection; autoimmune disease; haematopoietic disorder; therapy;
KW EPO; human; chimeric protein; stem cell expansion; tumour;

XX
OS
Homo sapiens.

XX	Key	Location/Qualifiers
FH		

FT Misc-difference 1..6 /notes "1-6 amino acids of the N-terminus are

FT	optionally deleted"
FT	Misc-difference 162 166

FT "1-5 amino acids of the C-terminus are
FT /note= "optionally deleted"

FT Misc-difference 23..24

Misc-difference 24..25

FT Misc-difference 25..26

FT Misc-difference 26..27

FT Misc-difference 27..28

FT Misc-difference 28..29

FT Misc-difference 29...30

FT Misc-difference 30..31

FI	/note=	possible positions of new C- and N-termini
FT	Misc-difference	31..32

FT possible positions of new C- and N-termini.
/note^{am} Misc-difference 32...33

FT	Misc-difference	/note=	possible positions of new C- and N-termini
33			
34			

F1	/note=	"possible positions of new C- and N-termini"
F1	Misc-difference	34 35

FT /note= "possible positions of new C- and N-termini"
FT Misc-difference 35 36

FT	"possible positions of new C- and N-termini."
FT	/note=
FT	Misc-difference
	36 37

FT /note= "possible positions of new C- and N-termini."

FT Misc-difference 37..38 /note= "possible positions of new C- and N-termini"
 FT FT
 FT Misc-difference 38..39 /note= "possible positions of new C- and N-termini"
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 FT Misc-difference 41..42 /note= "possible positions of new C- and N-termini"
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 FT Misc-difference 131..132 /note= "possible positions of new C- and N-termini"
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 FT FT
 XX WO9817810-A2.
 XX 30-APR-1998.
 XX 23-OCT-1997; 97WO-US20037.
 XX 25-OCT-1996; 96US-0029629.
 PR (SEAR) SEARLE & CO G D.
 XX Feng Y, McKearn JP, McWherter CA, Minnerly JC, Minster NI;
 PI Staten NR, Streeter PR, Summers NL, Woulfe SL;
 XX WPI; 1998-261504/23.
 DR Multi-functional chimeric haematopoietic receptor agonist - useful
 PT to treat haematopoietic disorders, tumours, infections or autoimmune
 PT diseases
 XX Claim 1; Page 762; 841pp; English.
 XX A human erythropoietin (EPO) receptor agonist polypeptide comprises
 CC a modified EPO amino acid sequence of the formula provided in
 CC AAW77780, in which the N-terminus is joined to the C-terminus directly
 CC or via a linker, the polypeptide having new C- and N-termini at one
 CC of the positions indicated. Novel claimed multi-functional chimeric
 CC haematopoietic receptor agonists (see AAW77812-22) have the formula
 CC R1-L1-R2, R2-L1-R1, R1-R2 or R2-R1, where L is a linker and R1 and
 CC R2 are independently selected from: (a) the human EPO receptor
 CC agonist; (b) a human stem cell factor receptor agonist polypeptide
 CC (see AAW77781); (c) a human flt-3 receptor agonist polypeptide (see
 CC AAW77782); (d) a modified human granulocyte colony stimulating factor
 CC (G-CSF) polypeptide (see AAW77783); (e) modified human interleukin-3
 CC polypeptide (see AAW77784); (f) modified human c-mpl ligand polypeptide
 CC (see AAW77785); and (g) a factor selected from the group consisting of

Sequence 166 AA:

RESULT 13
ABB07030
ID ABB07030 standard; Protein; 166 AA.
YY

The present invention describes modified erythropoietin (EPO) genes and expression vectors comprising the genes. The present sequence represents a protein sequence from the present invention.

Sequence	166 AA;
Query Match	100.0%; Score 846; DB 21; Length 166;
Best Local Similarity	100.0%; Pred. No. 1.1e-96;
Matches 165; Conservative	0; Mismatches 0; Indels 0; Gaps

Db 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKRMEVQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGLSLTTLLRALGAQKEAIS 120
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGLSLTTLLRALGAQKEAIS 120
 QY 121 PPDAAASAPLRTITADTFRKLFVYSNLFRLGKLVKLYTGEACRTGD 165
 Db 121 PPDAAASAPLRTITADTFRKLFVYSNLFRLGKLVKLYTGEACRTGD 165

RESULT 14

AAE02641
 ID AAE02641 standard; Protein; 166 AA.

XX AC AAE02641;

XX DT 06-AUG-2001 (first entry)

XX DE Human erythropoietin (EPO) mature protein.

XX KW Human; erythropoietin; EPO; antianaemic; nephrotrophic; anti-HIV;
 KW vaccine; haemostatic; immunoglobulin; Ig; EPO deficient disease;
 KW anaemia; renal failure; Human Immunodeficiency Virus; HIV;
 KW haematopoietic growth factor.

XX OS Homo sapiens.

XX PN WO200136489-A2.

XX PD 25-MAY-2001.

XX PF 03-NOV-2000; 2000WO-EPI0843.

XX PR 12-NOV-1999; 99US-0164855.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Hartmann A, Brandt S, Rieke E, Sobel C, Lo K, Way JC, Gillies S;

XX DR WPI; 2001-367563/38.

XX DR N-PSDB; AAD06893.

XX PT Novel modified erythropoietin forms such as fusion proteins, comprising
 PT Fc portion of an immunoglobulin molecule and a target molecule having
 PT the biological activity of erythropoietin forms

XX PS Example 1; Page 22; 58pp; English.

XX CC The present sequence is human erythropoietin (EPO) mature protein. EPO
 CC has improved biological activity and an extended serum half life greater
 CC than 20 hours. The present invention relates to modified EPO forms such
 CC as fusion proteins comprising a Fc portion of an immunoglobulin (Ig)
 CC molecule and an EPO molecule (Fc-EPO). The Fc portion is fused covalently
 CC through its C-terminus directly or indirectly to the EPO molecule, and
 CC where the Fc portion as well as EPO portion may be modified or mutated.
 CC The invention also relates to non-fused EPO molecules which have a
 CC pattern of cysteines or disulphide bonding which is distinct from human
 CC or animal EPO. Pharmaceutical compositions containing EPO are useful in
 CC the treatment of EPO deficient diseases such as anaemia, renal failure,
 CC HIV infection, blood loss and chronic disease that can be treated with
 CC haematopoietic growth factor.

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 846; DB 22; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKRMEVQQA 60

Db 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKRMEVQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGLSLTTLLRALGAQKEAIS 120
 Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGLSLTTLLRALGAQKEAIS 120
 QY 121 PPDAAASAPLRTITADTFRKLFVYSNLFRLGKLVKLYTGEACRTGD 165
 Db 121 PPDAAASAPLRTITADTFRKLFVYSNLFRLGKLVKLYTGEACRTGD 165

RESULT 15

AAE06698
 ID AAE06698 standard; Protein; 166 AA.

XX AC AAE06698;

XX DT 06-APR-2001 (first entry)

XX DE Human erythropoietin protein #2.

XX KW Erythropoietin; EPO; reticulocytes; red blood cell;
 KW ethylene glycol; chronic renal failure; AIDS; cancer.

XX OS Homo sapiens.

XX PN WO200102017-A2.

XX PD 11-JAN-2001.

XX PF 28-JUN-2000; 2000WO-EP06009.

XX PR 02-JUL-1999; 99US-0142243.

XX PR 05-AUG-1999; 99US-0147452.

XX PR 30-AUG-1999; 99US-0151454.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Burg J, Hilger B, Josel H;

XX DR WPI; 2001-147051/15.

XX PT Novel erythropoietin-glycoprotein conjugate useful for treating
 PT diseases correlated with anemia in chronic renal failure patients, AIDS
 PT and for treating cancer, is linked to polyethylene glycol through
 PT linker

XX PS Claim 19; Fig 2; 40pp; English.

XX CC The present invention relates to a conjugate comprising, human
 CC erythropoietin glycoprotein (EPO) having at least one free
 CC amino group and having in vivo biological activity of causing
 CC an increase the production of reticulocytes and red blood cells,
 CC covalently linked to 1-3 lower-alkoxy poly(ethylene glycol) groups
 CC through a linker. The invention is useful for preparation of
 CC medicaments for the treatment of prophylaxis of disease correlated
 CC with anemia in chronic renal failure patients (CRF), AIDS and for
 CC the treatment of cancer patients undergoing chemotherapy.

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 846; DB 22; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.1e-86;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKRMEVQQA 60

Db 1 APPRLICDSRVLYRLLLEAKEAENITTCGAHCSLNENITVPDTKYNFYAWKRMEVQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGLSLTTLLRALGAQKEAIS 120

Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGLSLTTLLRALGAQKEAIS 120

QY 121 PPDAAASAPLRTITADTFRKLFVYSNLFRLGKLVKLYTGEACRTGD 165

Db 121 PPDAASAAPLRTTTADTERKLFVYSNFLRGKLYTGEACRTGD 165

Search completed: June 13, 2003, 15:03:44
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:03:00 ; Search time 22 Seconds
(without alignments)
220.672 Million cell updates/sec

Title: US-09-830-964-1

Perfect score: 846
Sequence: 1 APRRLCDRVLRLVLEAK.....SNFLRGLKLYTGACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	165	4	US-09-604-871-1
2	846	100.0	166	1	US-08-318-193-70
3	846	100.0	166	4	US-09-604-871-2
4	846	100.0	166	5	PCT-US94-04361-37
5	846	100.0	193	1	US-07-903-220-1
6	846	100.0	193	2	US-08-883-795A-34
7	843	99.6	412	4	US-09-366-009-34
8	830	98.1	166	5	PCT-US94-04361-45
9	764.5	90.4	165	5	PCT-US94-04361-38
10	759.5	89.8	165	5	PCT-US94-04361-39
11	713	84.3	166	5	PCT-US94-04361-41
12	701	82.9	166	5	PCT-US94-04361-44
13	689	81.4	166	5	PCT-US94-04361-40
14	678.5	80.2	167	5	PCT-US94-04361-42
15	678	80.1	168	5	PCT-US94-04361-43
16	193	22.8	36	5	PCT-US94-04361-50
17	128	15.1	27	5	PCT-US94-04361-51
18	114.5	13.6	34	5	PCT-US94-04361-52
19	107	12.5	21	5	PCT-US94-04361-49
20	103	12.2	20	2	US-08-759-599-9
21	103	12.2	20	4	US-09-294-457-9
22	101	11.9	20	5	PCT-US94-04361-58
23	92	10.9	332	4	US-08-875-533-66
24	91	10.8	17	1	US-08-232-513A-11
25	91	10.8	17	4	US-09-231-159-16
26	91	10.8	17	4	US-08-611-307-16
27	91	10.8	312	4	US-08-875-533-67

28	89	10.5	153	4	US-08-875-533-65	Sequence 65, Appl
29	89	10.5	165	1	US-08-413-803-29	Sequence 29, Appl
30	89	10.5	174	3	US-08-471-045-56	Sequence 56, Appl
31	89	10.5	174	3	US-08-469-712A-56	Sequence 56, Appl
32	89	10.5	174	4	US-08-446-871-56	Sequence 56, Appl
33	89	10.5	174	4	US-08-468-910-56	Sequence 56, Appl
34	89	10.5	174	4	US-08-761-907-56	Sequence 56, Appl
35	89	10.5	174	5	PCT-US95-03776-27	Sequence 27, Appl
36	89	10.5	195	1	US-08-388-779A-4	Sequence 4, Appl
37	89	10.5	195	1	US-08-591-070A-4	Sequence 4, Appl
38	89	10.5	195	2	US-08-927-855-4	Sequence 4, Appl
39	89	10.5	285	4	US-08-875-533-69	Sequence 69, Appl
40	89	10.5	285	4	US-08-875-533-70	Sequence 70, Appl
41	89	10.5	288	4	US-08-875-533-71	Sequence 71, Appl
42	89	10.5	288	4	US-08-875-533-73	Sequence 73, Appl
43	89	10.5	332	4	US-08-875-533-22	Sequence 22, Appl
44	89	10.5	332	5	PCT-US95-03776-25	Sequence 25, Appl
45	89	10.5	353	1	US-08-330-517-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-604-871-1
; Sequence 1, Application US/09604871
; Patent No. 6340742
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Hilger, Bernd
; APPLICANT: Joesel, Hans-Peter
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1098 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,871
; CURRENT FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/151,454
; PRIOR FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: 60/147,452
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/142,243
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-871-1

Query Match 100.0%; Score 846; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.3e-100;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	APRRLCDRVLRLVLEAKAEENITTCGAHCNSLNENITVPTDKVNFYAKRMEVGQQA	60
DB	1	APRRLCDRVLRLVLEAKAEENITTCGAHCNSLNENITVPTDKVNFYAKRMEVGQQA	60
QY	61	VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGRLSLTTLRALCAQKEAIS	120
DB	61	VEVWQGLALLSEAVLRGQALLVNSQPWEPLQHLHVDKAVSGRLSLTTLRALCAQKEAIS	120
QY	121	PPDAASAPLRTITADTFKRLFRVSNFLRGKLYTGACRTGD	165
DB	121	PPDAASAPLRTITADTFKRLFRVSNFLRGKLYTGACRTGD	165

RESULT 2

US-08-318-193-70
; Sequence 70, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.

;; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
;; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
;; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
;; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
;; NUMBER OF SEQUENCES: 91
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 1800 Diagonal Road, Suite 500
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22313-0299
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/318,193
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/935,314
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 18740/116 CACO
;; TELEPHONE: (703)836-9300
;; TELEFAX: (703)683-4109
;; TELEX: 899149
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 166 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-318-193-70

Query Match 100.0%; Score 846; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.3e-100;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFKYAKRMVEVGQQA 60
|||||
Db 1 APRRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFKYAKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
|||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKCLKLYTGEACRTGD 165
|||||
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKCLKLYTGEACRTGD 165

RESULT 3
US-09-604-871-2
;; Sequence 2, Application US/09604871
;; Patent No. 6340742
;; GENERAL INFORMATION:
;; APPLICANT: Burg, Josef
;; APPLICANT: Hilger, Bernd
;; APPLICANT: Josel, Hans-Peter
;; FILE OF INVENTION: ERYTHROPOIETIN CONJUGATES
;; CURRENT APPLICATION NUMBER: US/09/604,871
;; CURRENT FILING DATE: 2000-06-28
;; PRIOR APPLICATION NUMBER: 60/151,454
;; PRIOR FILING DATE: 1999-08-30
;; PRIOR APPLICATION NUMBER: 60/147,452

;; PRIOR FILING DATE: 1999-08-05
;; PRIOR APPLICATION NUMBER: 60/142,243
;; PRIOR FILING DATE: 1999-07-02
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 166
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-604-871-2

Query Match 100.0%; Score 846; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.3e-100;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFKYAKRMVEVGQQA 60
|||||
Db 1 APRRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFKYAKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
|||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKCLKLYTGEACRTGD 165
|||||
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKCLKLYTGEACRTGD 165

RESULT 4
PCT-US94-04361-37
;; Sequence 37, Application PC/TUS9404361
;; GENERAL INFORMATION:
;; APPLICANT: Brigham and Women's Hospital
;; APPLICANT: 75 Francis Street
;; APPLICANT: Boston, MA 02115
;; APPLICANT: Bunn, H. Franklin
;; APPLICANT: Wen, Danyl
;; APPLICANT: Showers, Mark O.
;; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
;; NUMBER OF SEQUENCES: 59
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/04361
;; FILING DATE: Herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/049,802
;; FILING DATE: 21-APR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cimbala, Michele A.
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 0627.336PC01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 166 amino acids
;; TYPE: amino acid
;; TOPOLOGY: both
PCT-US94-04361-37

Query Match 100.0%; Score 846; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 5.3e-100; Indels 0; Gaps 0;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKVNFAWKRMVEVQQA 60
DB 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKVNFAWKRMVEVQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVSNFLRGKCLKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVSNFLRGKCLKLYTGEACRTGD 165

RESULT 5

US-07-903-220-1
; Sequence 1, Application US/07903220
; Patent No. 532837
; GENERAL INFORMATION:
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
; TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Paul H. Heller
; STREET: Kenyon & Kenyon, One Broadway
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/903.220
; FILING DATE: 19920731
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: 1248/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-1776
; TELEFAX: (202) 429-0796
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

US-07-903-220-1

Query Match 100.0%; Score 846; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.8e-100;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKVNFAWKRMVEVQQA 60
DB 28 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKVNFAWKRMVEVQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 147

QY 121 PPDAASAAPLRTITADTFKRLFRVSNFLRGKCLKLYTGEACRTGD 165
DB 148 PPDAASAAPLRTITADTFKRLFRVSNFLRGKCLKLYTGEACRTGD 192

RESULT 6

US-08-883-795A-34
; Sequence 34, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-883-795A-34

Query Match 100.0%; Score 846; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.8e-100;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKVNFAWKRMVEVQQA 60
DB 28 APPRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKVNFAWKRMVEVQQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVSNFLRGKCLKLYTGEACRTGD 165
DB 148 PPDAASAAPLRTITADTFKRLFRVSNFLRGKCLKLYTGEACRTGD 192

RESULT 7

US-09-366-009-34
; Sequence 34, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu

;; Kato, Ikunoshin
;; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
;; CELLS WITH RETROVIRUS
;; NUMBER OF SEQUENCES: 39
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: WEISER & ASSOCIATES
;; STREET: 230 South Fifteenth Street, Suite 500
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19102

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/366,009
;; FILING DATE: 02-Aug-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/809,156
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: JP 294382/1995
;; FILING DATE: 13-NOV-1995
;; APPLICATION NUMBER: JP 051847/1996
;; FILING DATE: 08-MAR-1996

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weiser, Gerard J.
;; REGISTRATION NUMBER: 19,763
;; REFERENCE/DOCKET NUMBER: 977.6507P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-875-8383
;; TELEFAX: 215-875-8394

;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 412 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-09-366-009-34
Query Match 99.6%; Score 843; DB 4; Length 412;
Best Local Similarity 99.4%; Pred. No. 5.5e-99;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCNENITVPDVKVNFYAKRMVGVQQA 60
Db 233 APRRLICDSRVRLRYLLEAKEAENITTCGAHCNENITVPDVKVNFYAKRMVGVQQA 292
QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
Db 293 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 352
QY 121 PPDASAAPLRTITADTRFKLFRVYSNPLRGKLYTGEACRTGD 165
Db 353 PPDASAAPLRTITADTRFKLFRVYSNPLRGKLYTGEACRTGD 397

RESULT 8

PCT-US94-04361-45

; Sequence 45, Application PC/TUS9404361

; GENERAL INFORMATION:

; APPLICANT: Brigham and Women's Hospital

; APPLICANT: 75 Francis Street

; APPLICANT: Boston, MA 02115

; APPLICANT: Bunn, H. Franklin

; APPLICANT: Wen, Danyi

; APPLICANT: Showers, Mark O.

; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced

; TITLE OF INVENTION: Activity

;; NUMBER OF SEQUENCES: 59
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005-3934

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/04361
;; FILING DATE: Herewith
;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/049,802
;; FILING DATE: 21-APR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cimbala, Michele A.
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 0627.336PC01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540

;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 166 amino acids
;; TYPE: amino acid
;; TOPOLOGY: both
;; PCT-US94-04361-45

Query Match 98.1%; Score 830; DB 5; Length 166;
Best Local Similarity 98.8%; Pred. No. 5.9e-98;
Matches 163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCNENITVPDVKVNFYAKRMVGVQQA 60
Db 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCNENITVPDVKVNFYAKRMVGVQQA 60
QY 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTRFKLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDASAAPLRTITADTRFKLFRVYSNPLRGKLYTGEACRTGD 165

RESULT 9

PCT-US94-04361-38

; Sequence 38, Application PC/TUS9404361

; GENERAL INFORMATION:

; APPLICANT: Brigham and Women's Hospital

; APPLICANT: 75 Francis Street

; APPLICANT: Boston, MA 02115

; APPLICANT: Bunn, H. Franklin

; APPLICANT: Wen, Danyi

; APPLICANT: Showers, Mark O.

; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced

; TITLE OF INVENTION: Activity

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; PCT-US94-04361-39
;
; Query Match 89.8%; Score 759.5; DB 5; Length 165;
; Best Local Similarity 90.3%; Pred. No. 5.9e-89;
; Matches 149; Conservative 9; Mismatches 6; Indels 1; Gaps 1;
;
; QY 1 APPRLCDRSVRLRYLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAKRMVEVGQA 60
; Db 1 APPRLVCDRSVRLRYLLEAKEAENVTMGCSSECSLNENITVPDTKVNFYAKRMVEVGQA 60
;
; QY 61 VEVWQGLLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGRLSTTLRLALGAQKEAIS 120
; Db 61 VEVWQGLLSEAVLRGQAVLNSQPFEPQLHMDKAISGRLSTTLRLALGAQ-ETALS 119
;
; QY 121 PPDAAASAPLRTITADTFKRLFRVYSNFLRGKGLKLYTGEACRTGD 165
; Db 120 LPDAAASAPLRTITADTFCKLFRVYSNFLRGKGLKLYTGEACRRGD 164
;
; RESULT 11
; PCT-US94-04361-44
; Sequence 44, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wen, Danyi
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
;

```

```

; TYPE: amino acid
; TOPOLOGY: both
PCT-US94-04361-44

Query Match      84.3%; Score 713; DB 5; Length 166;
Best Local Similarity 84.2%; Pred. No. 5.2e-83;
Matches 139; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKRMVEGQQA 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKRMVEGQQA 60

Qy 61 VEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEAIS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEAIS 120

Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165

RESULT 13
PCT-US94-04361-40
; Sequence 40, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wen, Danyi
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2500
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: both
PCT-US94-04361-40

Query Match      81.4%; Score 689; DB 5; Length 166;
Best Local Similarity 80.0%; Pred. No. 6.1e-80;
Matches 132; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKRMVEGQQA 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKRMVEGQQA 60

Qy 61 VEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEAIS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEAIS 120

Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 PPDTTPAPLRTLTVDTFKRLFRVYANFLRGKLLKLYTGEVCRGD 165

; TYPE: amino acid
; TOPOLOGY: both
PCT-US94-04361-41

Query Match      84.3%; Score 713; DB 5; Length 166;
Best Local Similarity 84.2%; Pred. No. 5.2e-83;
Matches 139; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKRMVEGQQA 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKRMVEGQQA 60

Qy 61 VEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEAIS 120
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Db 61 VEVWQGLALLSEAVLRGOALLVNSQPWEPLQLHVDKAVSGRLSRTLLRALGAQKEAIS 120

Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165
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Db 121 LPEATSAAPLRTTVDTLCKLFRVYSNFLRGKLLKLYTGEACRTGD 165

RESULT 12
PCT-US94-04361-41
; Sequence 41, Application PC/TUS9404361
; GENERAL INFORMATION:
; APPLICANT: Brigham and Women's Hospital
; APPLICANT: 75 Francis Street
; APPLICANT: Boston, MA 02115
; APPLICANT: Bunn, H. Franklin
; APPLICANT: Wen, Danyi
; APPLICANT: Showers, Mark O.
; TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04361
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,802
; FILING DATE: 21-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627.336PC01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2500
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: both
PCT-US94-04361-41

Query Match      82.9%; Score 701; DB 5; Length 166;
Best Local Similarity 82.4%; Pred. No. 1.8e-81;
Matches 136; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAWKRMVEGQQA 60
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RESULT 14

PCT-US94-04361-42
Sequence 42, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyl
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION/DOCKET NUMBER: 0627.336PC01
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-42

Query Match 80.2%; Score 678.5; DB 5; Length 167;
Best Local Similarity 81.3%; Pred. No. 1.3e-78;
Matches 135; Conservative 9; Mismatches 21; Indels 1; Gaps 1;
Qy 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCNENITVPDTKYNFYANKRMEVQQA 60
Db 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCNENITVPDTKYNFYANKRMEVQQA 60
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKAEIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKAEIS 120
Qy 121 PPDA--SAAPLRTITADTFKRLFRVYSNFLRGKLLTYTGEACRTGD 165
Db 121 LPDATPSAAPLRTITADTFKRLFRVYSNFLRGKLLTYTGEACRTGD 166

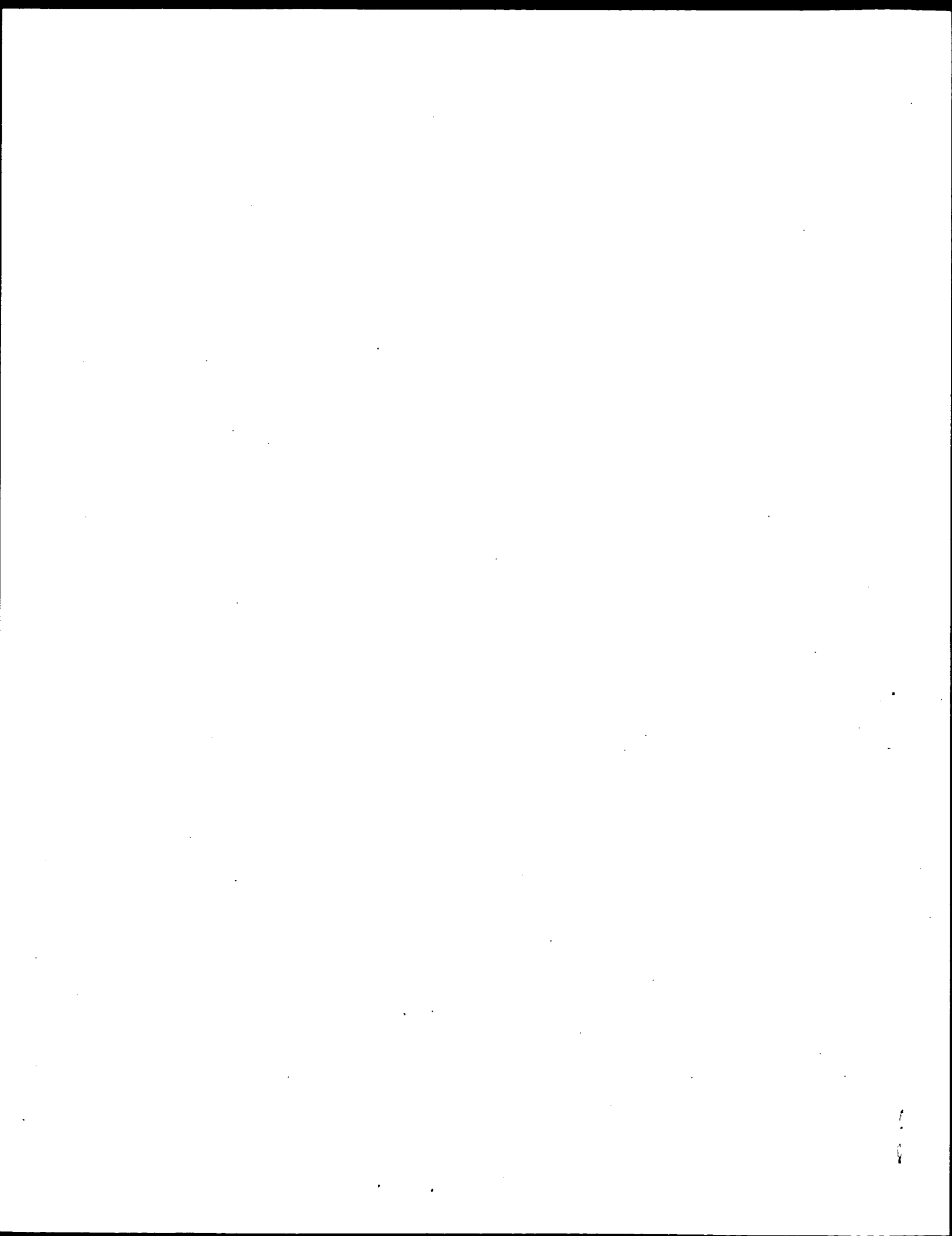
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PCT-US94-04361-43
Sequence 43, Application PC/TUS9404361
GENERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyl

APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION/DOCKET NUMBER: 0627.336PC01
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: both
PCT-US94-04361-43

Query Match 80.1%; Score 678; DB 5; Length 168;
Best Local Similarity 82.0%; Pred. No. 1.6e-78;
Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;
Qy 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCNENITVPDTKYNFYANKRMEVQQA 60
Db 1 APPRLICDSRVLYRLLEAKAEENITTCAGHCNENITVPDTKYNFYANKRMEVQQA 60
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKAEIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAKAEIS 120
Qy 121 PPDA--ASAPLRTITADTFKRLFRVYSNFLRGKLLTYTGEACRTGD 165
Db 121 LPDASPSSATPLRTFAVDTLCKLFRVYSNFLRGKLLTYTGEACRRRD 167

Search completed: June 13, 2003, 15:05:04
Job time : 24 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:04:47 ; Search time 47 Seconds
(without alignments)
375.342 Million cell updates/sec

Title: US-09-830-964-1
Perfect score: 846
Sequence: 1 APPRLICDSRVLELYLEAK.....SNFLRGKLYTGEACRTGD 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues
Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	846	100.0	165	9 US-10-241-356-1	Sequence 1, Appli
2	846	100.0	165	9 US-09-945-517-1	Sequence 1, Appli
3	846	100.0	165	10 US-09-853-731-1	Sequence 1, Appli
4	846	100.0	165	12 US-10-014-363-1	Sequence 1, Appli
5	846	100.0	166	9 US-10-241-356-2	Sequence 2, Appli
6	846	100.0	166	10 US-09-853-731-2	Sequence 2, Appli
7	846	100.0	166	12 US-10-014-363-2	Sequence 2, Appli
8	846	100.0	169	12 US-10-014-363-4	Sequence 4, Appli
9	846	100.0	174	12 US-10-014-363-3	Sequence 3, Appli
10	846	100.0	174	12 US-10-014-363-5	Sequence 5, Appli
11	846	100.0	193	9 US-10-113-824-2	Sequence 4, Appli
12	846	100.0	193	9 US-09-813-775C-4	Sequence 4, Appli
13	846	100.0	435	9 US-09-932-812-22	Sequence 22, Appli
14	846	100.0	436	9 US-09-932-812-18	Sequence 18, Appli
15	846	100.0	437	9 US-09-932-812-20	Sequence 20, Appli
16	843	99.6	412	9 US-09-775-964-34	Sequence 34, Appli
17	838	99.1	193	9 US-09-813-775C-2	Sequence 2, Appli
18	834	98.6	133	9 US-09-813-775C-5	Sequence 5, Appli
19	825	97.5	166	9 US-09-813-775C-30	Sequence 30, Appli

20	825	97.5	193	9	US-09-813-775C-46	Sequence 46, Appli
21	824	97.4	166	9	US-09-813-775C-22	Sequence 22, Appli
22	824	97.4	166	9	US-09-813-775C-32	Sequence 32, Appli
23	824	97.4	193	9	US-09-813-775C-38	Sequence 38, Appli
24	824	97.4	193	9	US-09-813-775C-48	Sequence 48, Appli
25	822	97.2	166	9	US-09-813-775C-20	Sequence 20, Appli
26	822	97.2	166	9	US-09-813-775C-24	Sequence 24, Appli
27	822	97.2	193	9	US-09-813-775C-36	Sequence 36, Appli
28	822	97.2	193	9	US-09-813-775C-40	Sequence 40, Appli
29	821	97.0	166	9	US-09-813-775C-26	Sequence 26, Appli
30	821	97.0	166	9	US-09-813-775C-31	Sequence 31, Appli
31	821	97.0	193	9	US-09-813-775C-42	Sequence 42, Appli
32	821	97.0	193	9	US-09-813-775C-47	Sequence 47, Appli
33	820	96.9	166	9	US-09-813-775C-23	Sequence 23, Appli
34	820	96.9	166	9	US-09-813-775C-23	Sequence 23, Appli
35	820	96.9	166	9	US-09-813-775C-28	Sequence 28, Appli
36	820	96.9	166	9	US-09-813-775C-33	Sequence 33, Appli
37	820	96.9	193	9	US-09-813-775C-34	Sequence 34, Appli
38	820	96.9	193	9	US-09-813-775C-39	Sequence 39, Appli
39	820	96.9	193	9	US-09-813-775C-44	Sequence 44, Appli
40	820	96.9	193	9	US-09-813-775C-49	Sequence 49, Appli
41	818	96.7	166	9	US-09-813-775C-21	Sequence 21, Appli
42	818	96.7	166	9	US-09-813-775C-25	Sequence 25, Appli
43	818	96.7	193	9	US-09-813-775C-37	Sequence 37, Appli
44	818	96.7	193	9	US-09-813-775C-41	Sequence 41, Appli
45	817	96.6	166	9	US-09-813-775C-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1
US-10-241-356-1
; Sequence 1, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-1

Query Match	100.0%	Score	846	DB	9	Length	165
Best Local Similarity	100.0%	Pred. No.	8.7e-84				
Matches	165	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMVEVGQQA	60				
Db	1	APPRLICDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMVEVGQQA	60				
QY	61	VEVWGLALLSEAVLRGQALLVNSQNPWEPLQHLVDKAVSGLSRLTTLRLALGAKQKAIS	120				
Db	61	VEVWGLALLSEAVLRGQALLVNSQNPWEPLQHLVDKAVSGLSRLTTLRLALGAKQKAIS	120				
QY	121	PPDAASAAPLRTITADTFRKLFPRVSNFLRGKLYTGEACRTGD	165				
Db	121	PPDAASAAPLRTITADTFRKLFPRVSNFLRGKLYTGEACRTGD	165				
RESULT 2							
US-09-945-517-1							
; Sequence 1, Application US/09945517							
; Publication No. US20030104996A1							
; GENERAL INFORMATION:							

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; APPLICANT: Li, Tiansheng
; APPLICANT: Chang, Byeong
; APPLICANT: Sloey, Christopher
; TITLE OF INVENTION: L-METHIONINE AS A STABILIZER FOR NESP/EPO IN HSA-FREE FORMULATION
; FILE REFERENCE: A-803
; CURRENT APPLICATION NUMBER: US/09/945,517
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-945-517-1

Query Match
Best Local Similarity 100.0%; Score 846; DB 9; Length 165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
Db 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165

RESULT 3
US-09-853-731-1
; Sequence 1, Application US/09853731
; Patent No. US20020037841A1
; GENERAL INFORMATION:
; APPLICANT: Papadimitriou, Apollon
; TITLE OF INVENTION: Erythropoietin Composition
; FILE REFERENCE: 20619 US
; CURRENT APPLICATION NUMBER: US/09/853,731
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP/00110355.5
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-731-1

Query Match
Best Local Similarity 100.0%; Score 846; DB 10; Length 165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165

RESULT 4
US-10-014-363-1
; Sequence 1, Application US/10014363
; Patent No. US20020115833A1
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; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-363-1

Query Match
Best Local Similarity 100.0%; Score 846; DB 12; Length 165;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
Db 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165

RESULT 5
US-10-241-356-2
; Sequence 2, Application US/10241356
; Publication No. US2003007753A1
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241,356
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: EP 01122555.4
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-356-2

Query Match
Best Local Similarity 100.0%; Score 846; DB 9; Length 166;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
Db 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFYAKRMEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKLYTGEACRTGD 165
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RESULT 6
 US-09-853-731-2
 ; Sequence 2, Application US/09853731
 ; Patent No. US20020037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Papadimitriou, Apollon
 ; TITLE OF INVENTION: Erythropoietin Composition
 ; FILE REFERENCE: 20619 US
 ; CURRENT APPLICATION NUMBER: US/09/853,731
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: EP/00110355.5
 ; PRIOR FILING DATE: 2000-05-15
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 166
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-853-731-2
 Query Match 100.0%; Score 846; DB 10; Length 166;
 Best Local Similarity 100.0%; Pred. No. 8.7e-84;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 APRRLICDSRVLYRLLEAKEAENITTCACAEHCNSLNENITVPDTKVNFYAKRMEVQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLLTLLRALGAQKEAIS 120
 QY 121 PPDAASAAPLRTITADTFRKLFVRYNSFLRGKCLKLYTGEACRTGD 165
 DB 121 PPDAASAAPLRTITADTFRKLFVRYNSFLRGKCLKLYTGEACRTGD 165
 RESULT 7
 US-10-014-363-2
 ; Sequence 2, Application US/10014363
 ; Patent No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Fischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 166
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-014-363-2
 Query Match 100.0%; Score 846; DB 12; Length 166;
 Best Local Similarity 100.0%; Pred. No. 8.7e-84;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYRLLEAKEAENITTCACAEHCNSLNENITVPDTKVNFYAKRMEVQQA 60
 DB 1 APRRLICDSRVLYRLLEAKEAENITTCACAEHCNSLNENITVPDTKVNFYAKRMEVQQA 60
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLLTLLRALGAQKEAIS 120
 DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFRKLFVRYNSFLRGKCLKLYTGEACRTGD 165
 DB 121 PPDAASAAPLRTITADTFRKLFVRYNSFLRGKCLKLYTGEACRTGD 165
 RESULT 8
 US-10-014-363-4
 ; Sequence 4, Application US/10014363
 ; Patent No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Fischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 169
 ; TYPE: PRT
 ; ORGANISM: CHO/dhfr-
 US-10-014-363-4
 Query Match 100.0%; Score 846; DB 12; Length 169;
 Best Local Similarity 100.0%; Pred. No. 9e-84;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYRLLEAKEAENITTCACAEHCNSLNENITVPDTKVNFYAKRMEVQQA 60
 DB 4 APRRLICDSRVLYRLLEAKEAENITTCACAEHCNSLNENITVPDTKVNFYAKRMEVQQA 63
 QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLLTLLRALGAQKEAIS 120
 DB 64 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLLTLLRALGAQKEAIS 123
 QY 121 PPDAASAAPLRTITADTFRKLFVRYNSFLRGKCLKLYTGEACRTGD 165
 DB 124 PPDAASAAPLRTITADTFRKLFVRYNSFLRGKCLKLYTGEACRTGD 168
 RESULT 9
 US-10-014-363-3
 ; Sequence 3, Application US/10014363
 ; Patent No. US20020115833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burg, Josef
 ; APPLICANT: Engel, Alfred
 ; APPLICANT: Franze, Reinhard
 ; APPLICANT: Hilger, Bernd
 ; APPLICANT: Schurig, Hartmut Ernst
 ; APPLICANT: Fischer, Wilhelm
 ; APPLICANT: Wozny, Manfred
 ; TITLE OF INVENTION: Erythropoietin Conjugates
 ; FILE REFERENCE: Case 20805
 ; CURRENT APPLICATION NUMBER: US/10/014,363
 ; CURRENT FILING DATE: 2001-12-11
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: CHO/dhfr-
 US-10-014-363-3
 Query Match 100.0%; Score 846; DB 12; Length 174;
 Best Local Similarity 100.0%; Pred. No. 9.3e-84;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 60
DB 9 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 68
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 165
DB 129 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 173

RESULT 10
US-10-014-363-5
; Sequence 5, Application US/10014363
; Patent No. US20020115833A1
; GENERAL INFORMATION:
; APPLICANT: Burg, Josef
; APPLICANT: Engel, Alfred
; APPLICANT: Franze, Reinhard
; APPLICANT: Hilger, Bernd
; APPLICANT: Schurig, Hartmut Ernst
; APPLICANT: Tischer, Wilhelm
; APPLICANT: Wozny, Manfred
; TITLE OF INVENTION: Erythropoietin Conjugates
; FILE REFERENCE: Case 20805
; CURRENT APPLICATION NUMBER: US/10/014,363
; CURRENT FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 174
; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-5

Query Match
Best Local Similarity 100.0%; Score 846; DB 12; Length 174;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 60
DB 9 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 68
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 69 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 128
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 165
DB 129 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 173

RESULT 11
US-10-113-824-2
; Sequence 2, Application US/10113824
; Publication No. US20030050269A1
; GENERAL INFORMATION:
; APPLICANT: Escary, Jean-Louis
; TITLE OF INVENTION: NEW POLYNUCLEOTIDES AND POLYPEPTIDES OF THE ERYTHROPOIETIN GENE
; FILE REFERENCE: 021349/0037
; CURRENT APPLICATION NUMBER: US/10/113,824
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: FR 0104603
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 60/343163
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/345,440
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/358,598

; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-824-2

Query Match
Best Local Similarity 100.0%; Score 846; DB 9; Length 193;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 60
DB 28 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 165
DB 148 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 192

RESULT 12
US-09-813-775C-4
; Sequence 4, Application US/09813775C
; Publication No. US20030054494A1
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. US20030054494A1el chimpanzee erythropoietin
; FILE REFERENCE: polypeptides and nucleic acids encoding the same
; CURRENT APPLICATION NUMBER: US/09/813,775C
; CURRENT FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/552265
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-775C-4

Query Match
Best Local Similarity 100.0%; Score 846; DB 9; Length 193;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 60
DB 28 APPRLICDSRVLYLLEAKAEANITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGOQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 165
DB 148 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGACRTGD 192

RESULT 13
US-09-932-812-22
; Sequence 22, Application US/09932812
; Publication No. US20030082749A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K

APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity
FILE REFERENCE: 02SUN2001
CURRENT APPLICATION NUMBER: US/09/932,812
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 435
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HuEPO-L-vFc gammal with a 27-amino acid leader peptide (Figure 2)
US-09-932-812-22

Query Match 100.0%; Score 846; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 3.4e-83;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQQA 60
DB 28 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQQA 87
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165
DB 148 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 192

RESULT 14
US-09-932-812-18
Sequence 18, Application US/09932812
Publication No. US20030082749A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity
FILE REFERENCE: 02SUN2001
CURRENT APPLICATION NUMBER: US/09/932,812
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 436
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2)
US-09-932-812-18

Query Match 100.0%; Score 846; DB 9; Length 436;
Best Local Similarity 100.0%; Pred. No. 3.4e-83;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQQA 60
DB 28 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQQA 87
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165
DB 148 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 192

RESULT 15
US-09-932-812-20
Sequence 20, Application US/09932812
Publication No. US20030082749A1
GENERAL INFORMATION:
APPLICANT: Sun, Lee-Hwei K
APPLICANT: Sun, Bill N
APPLICANT: Sun, Cecily R
TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with increased biological activity
FILE REFERENCE: 02SUN2001
CURRENT APPLICATION NUMBER: US/09/932,812
CURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 437
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2)
US-09-932-812-20

Query Match 100.0%; Score 846; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.4e-83;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQQA 60
DB 28 APRRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNIFYAKRMVEVGQQA 87
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
DB 88 VEVWQGLALLSEAVLRQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 147
QY 121 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 165
DB 148 PPDAASAAPLRTITADTFRKLFVYSNFLRGKLYTGACRTGD 192

Search completed: June 13, 2003, 15:13:52
Job time: 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:03:00 ; Search time 310 seconds
(without alignments)
343.164 Million cell updates/sec

Title: US-09-830-964-1

Perfect score: 846

Sequence: 1 APRRLICDSRLRYLLEAK.....SNFLRGKLYTGACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
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- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
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- 22: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	846	100.0	165	1 PCT-US99-26238-1	Sequence 1, Appli
2	846	100.0	165	1 PCT-US99-26240-1	Sequence 1, Appli
3	846	100.0	165	1 PCT-US99-26241-1	Sequence 1, Appli
4	846	100.0	165	18 US-09-426-566-1	Sequence 1, Appli
5	846	100.0	165	20 US-09-604-938-1	Sequence 1, Appli
6	846	100.0	165	22 US-09-830-964-1	Sequence 1, Appli

7	846	100.0	165	22	US-09-830-967-1	Sequence 1, Appli
8	846	100.0	165	22	US-09-830-968-1	Sequence 1, Appli
9	846	100.0	165	22	US-09-853-731-1	Sequence 1, Appli
10	846	100.0	165	22	US-09-854-018-1	Sequence 1, Appli
11	846	100.0	165	23	US-09-945-517-1	Sequence 1, Appli
12	846	100.0	165	24	US-10-014-363-1	Sequence 1, Appli
13	846	100.0	165	26	US-10-241-356-1	Sequence 1, Appli
14	846	100.0	166	1	PCT-US98-14497-2	Sequence 2, Appli
15	846	100.0	166	3	US-07-766-964A-3	Sequence 3, Appli
16	846	100.0	166	4	US-08-049-802-37	Sequence 37, Appli
17	846	100.0	166	6	US-08-223-263-7	Sequence 7, Appli
18	846	100.0	166	6	US-08-232-263A-7	Sequence 7, Appli
19	846	100.0	166	6	US-08-232-533-37	Sequence 7, Appli
20	846	100.0	166	6	US-08-249-376-7	Sequence 7, Appli
21	846	100.0	166	6	US-08-249-376A-7	Sequence 7, Appli
22	846	100.0	166	6	US-08-249-376B-7	Sequence 7, Appli
23	846	100.0	166	7	US-08-374-540-7	Sequence 7, Appli
24	846	100.0	166	8	US-08-422-020-7	Sequence 7, Appli
25	846	100.0	166	8	US-08-422-020A-7	Sequence 7, Appli
26	846	100.0	166	8	US-08-422-194-7	Sequence 7, Appli
27	846	100.0	166	8	US-08-422-194A-7	Sequence 7, Appli
28	846	100.0	166	8	US-08-422-548-7	Sequence 7, Appli
29	846	100.0	166	8	US-08-422-727-7	Sequence 7, Appli
30	846	100.0	166	8	US-08-422-727A-7	Sequence 7, Appli
31	846	100.0	166	8	US-08-423-194-7	Sequence 7, Appli
32	846	100.0	166	8	US-08-423-194A-7	Sequence 7, Appli
33	846	100.0	166	8	US-08-425-016-7	Sequence 7, Appli
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36	846	100.0	166	8	US-08-425-020-7	Sequence 7, Appli
37	846	100.0	166	8	US-08-425-020A-7	Sequence 7, Appli
38	846	100.0	166	8	US-08-425-095-7	Sequence 7, Appli
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40	846	100.0	166	8	US-08-433-098A-7	Sequence 7, Appli
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42	846	100.0	166	8	US-08-433-103-7	Sequence 7, Appli
43	846	100.0	166	8	US-08-433-103A-7	Sequence 7, Appli
44	846	100.0	166	8	US-08-433-766-7	Sequence 7, Appli
45	846	100.0	166	8	US-08-433-767-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

PCT-US99-26238-1
; Sequence 1, Application PC/TUS9926238
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeid Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1792.002PC02
; CURRENT APPLICATION NUMBER: PCT/US99/26238
; CURRENT FILING DATE: 1999-11-08
; EARLIER APPLICATION NUMBER: AR 99-01-00679
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 98-01-05609
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26238-1

Query Match 100.0%; Score 846; DB 1; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.2e-89;

Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
Db 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165
Db 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165

RESULT 2

PCT-US99-26240-1
; Sequence 1, Application PC/TUS9926240
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Method for the Massive Culture of Cells Producing Recombinant Human Erythropoietin
; FILE REFERENCE: 1792.004PC02
; CURRENT APPLICATION NUMBER: PCT/US99/26240
; CURRENT FILING DATE: 1999-11-08
; EARLIER APPLICATION NUMBER: AR 99-01-00681
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 98-01-05611
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26240-1

Query Match 100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
Db 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165
Db 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165

RESULT 3

PCT-US99-26241-1
; Sequence 1, Application PC/TUS9926241
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Methods of Purifying Recombinant Human Erythropoietin from Cell Culture Supernatants
; FILE REFERENCE: 1792.003PC02
; CURRENT APPLICATION NUMBER: PCT/US99/26241
; CURRENT FILING DATE: 1999-11-08
; EARLIER APPLICATION NUMBER: AR 99-01-00680
; EARLIER FILING DATE: 1999-02-23
; EARLIER APPLICATION NUMBER: AR 98-01-05610

; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0.
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-26241-1

Query Match 100.0%; Score 846; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
Db 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165
Db 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165

RESULT 4

US-09-426-566-1
; Sequence 1, Application US/09426566
; GENERAL INFORMATION:
; APPLICANT: Burke, Paul
; APPLICANT: Klumb, Lisa
; APPLICANT: Murphy, Keith
; APPLICANT: Herberger, John
; APPLICANT: French, Donna
; TITLE OF INVENTION: BIODEGRADABLE MICROPARTICLES FOR THE SUSTAINED DELIVERY OF NOVEL ERYTHROPOIETIN STIMULATING PROTEIN
; FILE REFERENCE: A-626
; CURRENT APPLICATION NUMBER: US/09/426,566
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: HUMAN
US-09-426-566-1

Query Match 100.0%; Score 846; DB 18; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
Db 1 APPRLICDSRVLELYLLEAKEAENITTCGAHCSLNENITVPDVKVNFYAWKRMVEVGQQA 60
QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSLTTLLRALGAQKEAIS 120
QY 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165
Db 121 PPDASAAPLRTITADTFKRLFRVYSNLFGRGKLKLYTGEACRTGD 165

RESULT 5

US-09-604-938-1
; Sequence 1, Application US/09604938
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/09/604,938

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; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-964-1

Query Match      100.0%; Score 846; DB 20; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVQQA 60
    |||||||
Db 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVQQA 60
    |||||||
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
    |||||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
    |||||||
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKCLKLYTGEACRTGD 165
    |||||||
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKCLKLYTGEACRTGD 165
    |||||||

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RESULT 6
US-09-830-964-1
; Sequence 1, Application US/09830964
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Methods of Purifying Recombinant Human
; TITLE OF INVENTION: Erythropoietin from Cell Culture Supernatants
; FILE REFERENCE: 1909.0030002
; CURRENT APPLICATION NUMBER: US/09/830,964
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00680
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05610
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-964-1

Query Match      100.0%; Score 846; DB 22; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVQQA 60
    |||||||
Db 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVQQA 60
    |||||||
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
    |||||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
    |||||||
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKCLKLYTGEACRTGD 165
    |||||||

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Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKCLKLYTGEACRTGD 165
    |||||||
RESULT 7
US-09-830-967-1
; Sequence 1, Application US/09830967
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0020002
; CURRENT APPLICATION NUMBER: US/09/830,967
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00679
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05609
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-967-1

Query Match      100.0%; Score 846; DB 22; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVQQA 60
    |||||||
Db 1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVQQA 60
    |||||||
Qy 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
    |||||||
Db 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
    |||||||
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKCLKLYTGEACRTGD 165
    |||||||
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNPLRGKCLKLYTGEACRTGD 165
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```

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RESULT 8
US-09-830-968-1
; Sequence 1, Application US/09830968
; GENERAL INFORMATION:
; APPLICANT: Sterrenbeld Biotechnologie North America, Inc.
; APPLICANT: Carcagno, Carlos Miguel
; APPLICANT: Criscuolo, Marcelo
; APPLICANT: Melo, Carlos
; APPLICANT: Vidal, Juan Alejandro
; TITLE OF INVENTION: Method for the Massive Culture of Cells
; TITLE OF INVENTION: Producing Recombinant Human Erythropoietin
; FILE REFERENCE: 1909.0040002
; CURRENT APPLICATION NUMBER: US/09/830,968
; CURRENT FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: AR 99-01-00681
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: AR 98-01-05611
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-968-1

Query Match      100.0%; Score 846; DB 22; Length 165;

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Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60
DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165

RESULT 9

US-09-853-731-1
: Sequence 1, Application US/09853731
: GENERAL INFORMATION:
: APPLICANT: Papadimitriou, Apollon
: TITLE OF INVENTION: Erythropoietin Composition
: FILE REFERENCE: 20619 US
: CURRENT APPLICATION NUMBER: US/09/853,731
: CURRENT FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: EP/00110355.5
: PRIOR FILING DATE: 2000-05-15
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 165
: TYPE: PRT
: ORGANISM: Homo sapiens

US-09-853-731-1

Query Match 100.0%; Score 846; DB 22; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60
DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165

RESULT 10

US-09-854-018-1
: Sequence 1, Application US/09854018
: GENERAL INFORMATION:
: APPLICANT: Herberger, John
: TITLE OF INVENTION: Secondary Drying of Microparticles Using Pressurized Carbon Dioxide
: FILE REFERENCE: A-786
: CURRENT APPLICATION NUMBER: US/09/854,018
: CURRENT FILING DATE: 2001-05-10
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 165
: TYPE: PRT
: ORGANISM: Human

US-09-854-018-1

Query Match 100.0%; Score 846; DB 22; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60
DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165

RESULT 11

US-09-945-517-1
: Sequence 1, Application US/09945517
: GENERAL INFORMATION:
: APPLICANT: Li, Tiansheng
: APPLICANT: Chang, Byeong
: APPLICANT: Sloey, Christopher
: TITLE OF INVENTION: L-METHIONINE AS A STABILIZER FOR NESP/EPO IN HSA-FREE FORMULATIONS
: FILE REFERENCE: A-803
: CURRENT APPLICATION NUMBER: US/09/945,517
: CURRENT FILING DATE: 2001-08-30
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 165
: TYPE: PRT
: ORGANISM: Homo sapiens

US-09-945-517-1

Query Match 100.0%; Score 846; DB 23; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60
DB 1 APPRLICDSRVLYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYAWKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165
DB 121 PPDAASAAPLRTITADTFKRLFRVYSNLFGRGKLYTGEACRTGD 165

RESULT 12

US-10-014-363-1
: Sequence 1, Application US/10014363
: GENERAL INFORMATION:
: APPLICANT: Burg, Josef
: APPLICANT: Engel, Alfred
: APPLICANT: Franze, Reinhard
: APPLICANT: Hilger, Bernd
: APPLICANT: Schurig, Hartmut Ernst
: APPLICANT: Tischer, Wilhelm
: APPLICANT: Wozny, Manfred
: TITLE OF INVENTION: Erythropoietin Conjugates
: FILE REFERENCE: Case 20805
: CURRENT APPLICATION NUMBER: US/10/014,363
: CURRENT FILING DATE: 2001-12-11
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 165
: TYPE: PRT
: ORGANISM: Homo sapiens

US-10-014-363-1

Query Match 100.0%; Score 846; DB 24; Length 165;

Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60
DB 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PDAAASAAPLRITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165
DB 121 PDAAASAAPLRITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165

RESULT 13
US-10-241-356-1
; Sequence 1, Application US/10241356
; GENERAL INFORMATION:
; APPLICANT: TISCHER, WILHELM
; TITLE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
; FILE REFERENCE: 20971
; CURRENT APPLICATION NUMBER: US/10/241.356
; PRIOR FILING DATE: 2002-09-11
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-241-356-1

Query Match 100.0%; Score 846; DB 26; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60
DB 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PDAAASAAPLRITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165
DB 121 PDAAASAAPLRITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165

RESULT 14
PCT-US98-14497-2
; Sequence 2, Application PC/TUS9814497
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: BB0011
; CURRENT APPLICATION NUMBER: PCT/US98/14497
; CURRENT FILING DATE: 1998-07-13
; EARLIER APPLICATION NUMBER: 60/052.516
; EARLIER FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-14497-2

Query Match 100.0%; Score 846; DB 1; Length 166;

Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60
DB 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

QY 121 PDAAASAAPLRITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165
DB 121 PDAAASAAPLRITADTFKRLFRVYSNFLRGKLLKLYTGEACRTGD 165

RESULT 15
US-07-766-964A-3
; Sequence 3, Application US/07766964A
; GENERAL INFORMATION:
; APPLICANT: Rosen, Jonathan I.
; TITLE OF INVENTION: HYBRID GROWTH FACTORS
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robert L. Minier
; STREET: 1 Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08933
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,964A
; FILING DATE: 19910926
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/589,958
; FILING DATE: 28-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stark, Michael
; REGISTRATION NUMBER: 32,495
; REFERENCE/DOCKET NUMBER: BCI-15
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-524-2817
; TELEFAX: 908-524-2808
; TELEX: 844-481
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-766-964A-3

Query Match 100.0%; Score 846; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60
DB 1 APRRLICDSRVLYRLLEAKAEENITTCAGHCSLNENITVPDTKVNFYANKRMEVGQQA 60

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
DB 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:03:51 ; Search time 108 Seconds
(without alignments) 389.731 Million cell up

Title: US-09-830-964-1

Perfect score: 846

Sequence: 1 APPRLICDSRVLERYLLEAK.....SNFLRGKCLKLYTGEACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155225 seqs, 255096386 residues

Total number of hits satisfying chosen parameters: 1155225

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

100% Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US60_US60_NEW_COMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	846	100.0	165	5	US-09-687-981-1		Sequence 1, Appli
2	846	100.0	165	6	US-10-293-551-1		Sequence 1, Appli
3	846	100.0	165	6	US-10-411-012-73		Sequence 73, Appl
4	846	100.0	165	6	US-10-411-026-73		Sequence 73, Appl
5	846	100.0	165	6	US-10-410-930-73		Sequence 73, Appl
6	846	100.0	165	6	US-10-410-945-73		Sequence 73, Appl
7	846	100.0	165	6	US-10-410-962-73		Sequence 73, Appl
8	846	100.0	165	6	US-10-410-980-73		Sequence 73, Appl
9	846	100.0	165	6	US-10-411-044-73		Sequence 73, Appl
10	846	100.0	165	6	US-10-411-049-73		Sequence 73, Appl
11	846	100.0	165	6	US-10-410-913-73		Sequence 73, Appl
12	846	100.0	165	6	US-10-411-037-73		Sequence 73, Appl
13	846	100.0	165	6	US-10-411-043-73		Sequence 73, Appl
14	846	100.0	165	6	US-10-410-897-73		Sequence 73, Appl
15	846	100.0	165	6	US-10-410-987-73		Sequence 73, Appl
16	846	100.0	166	5	US-09-708-506A-2		Sequence 2, Appli
17	846	100.0	166	6	US-10-293-551-2		Sequence 2, Appli
18	846	100.0	166	6	US-10-298-148-2		Sequence 2, Appli
19	846	100.0	166	6	US-10-400-377-2		Sequence 2, Appli
20	846	100.0	166	6	US-10-400-708-2		Sequence 2, Appli
21	846	100.0	166	6	US-10-360-101-227		Sequence 227, App
22	846	100.0	192	1	PCT-US02-40891-593		Sequence 593, App
23	846	100.0	192	1	PCT-US02-40891-594		Sequence 594, App
24	846	100.0	192	1	PCT-US02-40891-603		Sequence 603, App
25	846	100.0	192	1	PCT-US02-40891-1689		Sequence 1689, Ap
26	846	100.0	192	1	PCT-US02-40891-1690		Sequence 1690, Ap

ALIGNMENTS

RESULT 1

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US-09-687-981-1
; Sequence 1, Application US/09687981
; GENERAL INFORMATION:
; APPLICANT: Burke, Paul
; APPLICANT: Klumb, Lisa
; APPLICANT: Murphy, Keith
; APPLICANT: Herberger, John
; APPLICANT: French, Donna
; TITLE OF INVENTION: BIODEGRADABLE MICROPARTICLES FOR THE SUSTAINED DELIVERY OF NOV
; TITLE OF INVENTION: ERYTHROPOIETIN STIMULATING PROTEIN
; FILE REFERENCE: A-626A
; CURRENT APPLICATION NUMBER: US/09/687,981
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/426,566
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-687-981-1

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Query Match	100.0%;	Score 846;	DB 5;	Length 165;
Best Local Similarity	100.0%;	Pred. No. 7.2e-78;		
Matches 165:	Conservative	0:	Mismatches	0: Indels

1	APPRICDSRVRLRYLLEAKEAEENITTTGCAEHCSLNENITVPDTKNFYAWKRMVEGQQA	60
1	APPRICDSRVRLRYLLEAKEAEENITTTGCAEHCSLNENITVPDTKNFYAWKRMVEGQQA	60
61	VEVWQGLALLSEAVLRQGLLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS	120
61	VEVWQGLALLSEAVLRQGLLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS	120
121	PPDAASAPLRTITADTFRLKFRVYSNFRGKUKLYTGEACRTGD	165
121	PPDAASAPLRTITADTFRLKFRVYSNFRGKUKLYTGEACRTGD	165

RESULT 2

RES-01
US-10-293-551-1
; Sequence 1, Application US/10293551
; GENERAL INFORMATION:
; APPLICANT: Bailon, Pascal
; TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
; FILE REFERENCE: 1097 nonprovisional
; CURRENT APPLICATION NUMBER: US/10/293,551

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; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/604,938
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/166,151
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/151,548
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/150,225
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/142,254
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-551-1

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```

Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGQQA 60
   |||||
DB 1 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGQQA 60
   |||||
QY 61 VEWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
   |||||
DB 61 VEWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
   |||||
QY 121 PDAASAAPLRTITADTFKLFVYSNFRGKGLKLYTGEACRTGD 165
   |||||
DB 121 PDAASAAPLRTITADTFKLFVYSNFRGKGLKLYTGEACRTGD 165
   |||||

```

```

RESULT 3
US-10-411-012-73
; Sequence 73, Application US/10411012
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-012-73

```

```

Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGQQA 60
   |||||
DB 1 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGQQA 60
   |||||
QY 61 VEWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
   |||||
DB 61 VEWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
   |||||
QY 121 PDAASAAPLRTITADTFKLFVYSNFRGKGLKLYTGEACRTGD 165
   |||||
DB 121 PDAASAAPLRTITADTFKLFVYSNFRGKGLKLYTGEACRTGD 165
   |||||

```

```

RESULT 4
US-10-411-026-73
; Sequence 73, Application US/10411026
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY T
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-73

```

```

Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGQQA 60
   |||||
DB 1 APPRLICDSRVLYRYLLEAKAEENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGQQA 60
   |||||
QY 61 VEWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
   |||||
DB 61 VEWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGRLSLTLLRALGAQKEAIS 120
   |||||
QY 121 PDAASAAPLRTITADTFKLFVYSNFRGKGLKLYTGEACRTGD 165
   |||||
DB 121 PDAASAAPLRTITADTFKLFVYSNFRGKGLKLYTGEACRTGD 165
   |||||

```

RESULT 5


```
US-10-410-930-73
: Sequence 73, Application US/10410930
: GENERAL INFORMATION:
: APPLICANT: Neose Technologies, Inc.
: APPLICANT: DeFrees, Shawn
: APPLICANT: Zopf, David
: APPLICANT: Bayer, Robert
: APPLICANT: Hakes, David
: APPLICANT: Chen, Xi
: APPLICANT: Bowe, Catyn
: TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
: FILE REFERENCE: 040853-01-5056
: CURRENT APPLICATION NUMBER: US/10/410,930
: PRIOR FILING DATE: 2003-04-09
: PRIOR APPLICATION NUMBER: US 60/328,523
: PRIOR FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/344,692
: PRIOR FILING DATE: 2001-10-19
: PRIOR APPLICATION NUMBER: US 60/387,292
: PRIOR FILING DATE: 2002-06-07
: PRIOR APPLICATION NUMBER: US 60/391,777
: PRIOR FILING DATE: 2002-06-25
: PRIOR APPLICATION NUMBER: US 60/396,594
: PRIOR FILING DATE: 2002-08-16
: PRIOR APPLICATION NUMBER: US 60/404,249
: PRIOR FILING DATE: 2002-08-28
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: Patentin version 3.2
: SEQ ID NO 73
: LENGTH: 165
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-410-930-73

Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPLICDSRVLELYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFWYAWKRMVEVGOQA 60
Db 1 APPLICDSRVLELYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFWYAWKRMVEVGOQA 60
Qy 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 6
US-10-410-945-73
: Sequence 73, Application US/10410945
: GENERAL INFORMATION:
: APPLICANT: Neose Technologies, Inc.
: APPLICANT: DeFrees, Shawn
: APPLICANT: Zopf, David
: APPLICANT: Bayer, Robert
: APPLICANT: Hakes, David
: APPLICANT: Chen, Xi
: APPLICANT: Bowe, Catyn
: TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF ERYTHROPOIETIN
: FILE REFERENCE: 040853-01-5083
: CURRENT APPLICATION NUMBER: US/10/410,945
: PRIOR FILING DATE: 2003-04-09
: PRIOR APPLICATION NUMBER: US 60/328,523
: PRIOR FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/344,692
: PRIOR FILING DATE: 2001-10-19
```

```
US-10-410-962-73
: Sequence 73, Application US/10410962
: GENERAL INFORMATION:
: APPLICANT: Neose Technologies, Inc.
: APPLICANT: DeFrees, Shawn
: APPLICANT: Zopf, David
: APPLICANT: Bayer, Robert
: APPLICANT: Hakes, David
: APPLICANT: Chen, Xi
: APPLICANT: Bowe, Catyn
: TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
: FILE REFERENCE: 040853-01-5054
: CURRENT APPLICATION NUMBER: US/10/410,962
: PRIOR FILING DATE: 2003-04-09
: PRIOR APPLICATION NUMBER: US 60/328,523
: PRIOR FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/344,692
: PRIOR FILING DATE: 2001-10-19
: PRIOR APPLICATION NUMBER: US 60/387,292
: PRIOR FILING DATE: 2002-06-07
: PRIOR APPLICATION NUMBER: US 60/391,777
: PRIOR FILING DATE: 2002-06-25
: PRIOR APPLICATION NUMBER: US 60/396,594
: PRIOR FILING DATE: 2002-07-17
: PRIOR APPLICATION NUMBER: US 60/404,249
: PRIOR FILING DATE: 2002-08-16
: PRIOR APPLICATION NUMBER: US 60/407,527
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: Patentin version 3.2
: SEQ ID NO 73
: LENGTH: 165
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-410-962-73

Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APPLICDSRVLELYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFWYAWKRMVEVGOQA 60
Db 1 APPLICDSRVLELYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFWYAWKRMVEVGOQA 60
Qy 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
Db 61 VEVWQGLALLSEAVLRQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
Qy 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKRLFRVYSNFLRGKLYTGEACRTGD 165

RESULT 7
US-10-410-962-73
: Sequence 73, Application US/10410962
: GENERAL INFORMATION:
: APPLICANT: Neose Technologies, Inc.
: APPLICANT: DeFrees, Shawn
: APPLICANT: Zopf, David
: APPLICANT: Bayer, Robert
: APPLICANT: Hakes, David
: APPLICANT: Chen, Xi
: APPLICANT: Bowe, Catyn
: TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
: FILE REFERENCE: 040853-01-5054
: CURRENT APPLICATION NUMBER: US/10/410,962
: PRIOR FILING DATE: 2003-04-09
: PRIOR APPLICATION NUMBER: US 60/328,523
: PRIOR FILING DATE: 2001-10-10
: PRIOR APPLICATION NUMBER: US 60/344,692
: PRIOR FILING DATE: 2001-10-19
: PRIOR APPLICATION NUMBER: US 60/387,292
: PRIOR FILING DATE: 2002-06-07
: PRIOR APPLICATION NUMBER: US 60/391,777
: PRIOR FILING DATE: 2002-06-25
: PRIOR APPLICATION NUMBER: US 60/396,594
: PRIOR FILING DATE: 2002-07-17
: PRIOR APPLICATION NUMBER: US 60/404,249
: PRIOR FILING DATE: 2002-08-16
: PRIOR APPLICATION NUMBER: US 60/407,527
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: Patentin version 3.2
: SEQ ID NO 73
: LENGTH: 165
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-410-962-73
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Query Match      100.0%   Score 846;   DB 6;   Length 165;
Best Local Similarity 100.0%;   Pred. No. 7.2e-78;
Matches 165;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVGQQA 60
        |||||||
DB      1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVGQQA 60
        |||||||
QY      61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
        |||||||
DB      61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
        |||||||
QY      121 PPDAASAAPLRTITADTKFKLFRVYSNLFRLGKLYTGEACRTGD 165
        |||||||
DB      121 PPDAASAAPLRTITADTKFKLFRVYSNLFRLGKLYTGEACRTGD 165
        |||||||

RESULT 8
US-10-410-980-73
; Sequence 73, Application US/10410980
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2
; FILE REFERENCE: 040853-01-5066
; CURRENT APPLICATION NUMBER: US/10/410,980
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-980-73

Query Match      100.0%   Score 846;   DB 6;   Length 165;
Best Local Similarity 100.0%;   Pred. No. 7.2e-78;
Matches 165;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVGQQA 60
        |||||||
DB      1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVGQQA 60
        |||||||
QY      61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
        |||||||
DB      61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
        |||||||
QY      121 PPDAASAAPLRTITADTKFKLFRVYSNLFRLGKLYTGEACRTGD 165
        |||||||
DB      121 PPDAASAAPLRTITADTKFKLFRVYSNLFRLGKLYTGEACRTGD 165
        |||||||

RESULT 9
US-10-411-044-73
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```
; Sequence 73, Application US/10411044
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: BETA-GLUCOSIDASE: REMODELING AND GLYCOCONJUGATION OF
; TITLE OF INVENTION: BETA-GLUCOSIDASE
; FILE REFERENCE: 040853-01-5064
; CURRENT APPLICATION NUMBER: US/10/411,044
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-044-73

Query Match      100.0%   Score 846;   DB 6;   Length 165;
Best Local Similarity 100.0%;   Pred. No. 7.2e-78;
Matches 165;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVGQQA 60
        |||||||
DB      1 APPRLICDSRVLYRLLEAKAEENITTCGAHCSLNENITVPDTKVNFAWKRMVEVGQQA 60
        |||||||
QY      61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
        |||||||
DB      61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS 120
        |||||||
QY      121 PPDAASAAPLRTITADTKFKLFRVYSNLFRLGKLYTGEACRTGD 165
        |||||||
DB      121 PPDAASAAPLRTITADTKFKLFRVYSNLFRLGKLYTGEACRTGD 165
        |||||||

RESULT 10
US-10-411-049-73
; Sequence 73, Application US/10411049
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERO
; TITLE OF INVENTION: ALPHA
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
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US-10-410-913-73

```

US-10-411-043-73
; Sequence 73, Application US/10411043
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ANTI-TUMOR NECROSIS FACTOR ALPHA: REMODELING AND GLYCOCONJUGATION OF
; FILE REFERENCE: 040853-01-5075
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 10/411,043
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-043-73

Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APPRLICDSRVLELYLLEAKAEENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGQQA 60
      1 APPRLICDSRVLELYLLEAKAEENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGQQA 60
      61 VEVWGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
      61 VEVWGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
      121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
      121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165

RESULT 14
US-10-410-997-73
; Sequence 73, Application US/10410897
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: FACTOR IX: REMODELING AND GLYCOCONJUGATION OF FACTOR IX
; FILE REFERENCE: 040853-01-5058
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/10/410,897
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19

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; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-897-73

Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APPRLICDSRVLELYLLEAKAEENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGQQA 60
      1 APPRLICDSRVLELYLLEAKAEENITTCGAHCNSLNENITVPDTKVNFYAKRMEVGQQA 60
      61 VEVWGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
      61 VEVWGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
      121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
      121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165

RESULT 15
US-10-410-997-73
; Sequence 73, Application US/10410997
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION
; FILE REFERENCE: 040853-01-5059
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-997-73

```

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Query Match      100.0%; Score 846; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLERYLLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWKRMEVGQQA 60
Db 1 APPRLICDSRVLERYLLLEAKEAENITTCGAHCSLNENITVPDTKVNFYAWKRMEVGQQA 60
QY 61 VEVMOGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
Db 61 VEVMOGLALLSEAVLRGOALLVNSSQPWEPLQLHVDKAVSGLRSLTTLRALGAQKEAIS 120
QY 121 PPDAASAAPLRTITADTFKLFVYSNFLRGKCLKYTGEACRTGD 165
Db 121 PPDAASAAPLRTITADTFKLFVYSNFLRGKCLKYTGEACRTGD 165

```

Search completed: June 13, 2003, 15:12:17
Job time : 109 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:03:00 ; Search time 24 seconds
(without alignments)
660.924 Million cell updates/sec

Title: US-09-830-964-1

Perfect score: 846

Sequence: 1 APPRLICDSRVLYLEAK.....SNFLRGKLYTGEACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	100.0	193	1 ZUHU	erythropoietin pre
2	764.5	90.4	192	1 JQ0173	erythropoietin pre
3	759.5	89.8	192	1 I84613	erythropoietin pre
4	713	84.3	188	1 I46083	erythropoietin pre
5	701	82.9	192	1 S28148	erythropoietin pre
6	685.5	81.0	194	1 I46401	erythropoietin pre
7	681	80.5	192	1 A24902	erythropoietin pre
8	680.5	80.4	195	2 JC7699	erythropoietin - r
9	678	80.1	190	2 I46578	erythropoietin - p
10	638	75.4	175	2 I46199	erythropoietin - d
11	90	10.6	353	2 G02729	erythropoietin - h
12	89	10.5	353	2 I80105	thrombopoietin pre
13	88	10.4	323	2 AB0323	ribonucleoside-dip
14	87.5	10.3	346	2 AE0959	Solute binding rec
15	86	10.2	286	2 A55530	megakaryocyte grow
16	83	9.8	286	2 AI0443	probable 2-hydroxy
17	83	9.8	339	2 A83274	UDP-N-acetylpyruvo
18	80.5	9.5	3033	1 GNMVJ8	genome polyprotein
19	79.5	9.4	1829	2 T35681	probable sensory h
20	79	9.3	480	2 S56639	ribosomal protein
21	78.5	9.3	813	2 AF0526	ATP-dependent heli
22	78.5	9.3	897	2 A54096	EGF receptor subst
23	78	9.2	348	2 T35450	ABC transporter AT
24	78	9.2	455	2 H97693	methylamine utiliz
25	78	9.2	455	2 AG2919	conserved hypothet
26	77.5	9.2	747	1 S36741	probable copper-tr
27	77.5	9.2	242	2 AD1928	hypothetical prote
28	77	9.1	451	2 S75569	hypothetical prote
29	76.5	9.0	154	2 H82810	bacterioferritin x

RESULT 1

ZUHU

erythropoietin precursor [validated] - human

C:Species: Homo sapiens (man)

C>Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 08-Dec-2000

C:Accession: A01855; A24744; A25384; A22210; S56178

R:Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.;

Nature 313, 806-810, 1985

A>Title: Isolation and characterization of genomic and cDNA clones of human erythropo

A:Reference number: A01855; MUID:85137899; PMID:3838366

A:Accession: A01855

A:Molecule type: mRNA; DNA

A:Residues: 1-193 <JAC>

A:Cross-references: GB:X02157; GB:X02158

R:Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K

Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985

A>Title: Cloning and expression of the human erythropoietin gene.

A:Reference number: A24744; MUID:86067948; PMID:3865178

A:Accession: A24744

A:Molecule type: DNA

A:Residues: 1-193 <LIN>

A:Cross-references: GB:M11319; MUID:9182197; PIDN:AAA52400.1; PID:g182198

R:Lai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.

J. Biol. Chem. 261, 3116-3121, 1986

A>Title: Structural characterization of human erythropoietin.

A:Reference number: A25384; MUID:86140080; PMID:3949763

A:Accession: A25384

A:Molecule type: protein

A:Residues: 28-86, 'Q', 87-193 <LAI>

A:Experimental source: urine

A>Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal re

R:Yanagawa, S.; Hirade, K.; Ohnata, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.

J. Biol. Chem. 259, 2707-2710, 1984

A>Title: Isolation of human erythropoietin with monoclonal antibodies.

A:Reference number: A22210; MUID:84135751; PMID:6698989

A:Accession: A22210

A:Molecule type: protein

A:Residues: 28-29, 'X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>

R:Matsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.

Plant Mol. Biol. 27, 1163-1172, 1995

A>Title: Characterization of a human glycoprotein (erythropoietin) produced in cultur

A:Reference number: S56178; MUID:95284365; PMID:7766897

A:Accession: S56178

A:Molecule type: protein

A:Residues: 28-33, 'X', 35-37 <WTS>

C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live

C:Genetics:

A:Gene: GDB:EPO

A:Cross-references: GDB:119110; OMIM:133170

A:Map position: 7q21.3-7q22.1

A:introns: 5/1; 53/3; 82/3; 142/3

C:Function:

mandelate racemase
hypothetical prote
conserved hypothet
rLs beta (AF305057
ATP-dependent heli
RF2 protein - saim
thrombopoietin pre
ribonucleoside-dip
probable transport
hypothetical prote
GCN5 protein - hum
vacB protein XF198
WD-repeat family p
PSE1 protein - yea
NADH2 dehydrogenas
precorrin-6y C5,15

ALIGNMENTS

A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-193/Product: erythropoietin #status experimental <MAT>
 F:34-188/Disulfide bonds: #status experimental
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:153/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.08; Score 846; DB 1; Length 193;
 Best Local Similarity 100.08; Pred. No. 1.8e-74;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 60
 |||||
 Db 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 87
 |||||

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 |||||
 Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 147
 |||||

QY 121 PDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165
 |||||
 Db 148 PDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 192
 |||||

RESULT 2
 JQ0173
 erythropoietin precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: JQ0173
 R:Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; C
 Gene 44, 201-209; 1986
 A:Title: Monkey erythropoietin gene: cloning, expression and comparison with the human e
 A:Reference number: JQ0173; MUID:87055236; PMID:2877922
 A:Accession: JQ0173
 A:Molecule type: mRNA
 A:Residues: 1-192 <RES>
 A:Cross-references: GB:M18189; GB:M15818; GB:M15819; GB:M18188; NID:g342093; PIDN:AAA368
 A:Experimental source: kidney
 C:Comment: This protein is the principal hormone involved in the regulation of erythrocy
 C:Function: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
 C:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-192/Product: erythropoietin #status predicted <MAT>
 F:34-187,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 90.4%; Score 764.5; DB 1; Length 192;
 Best Local Similarity 91.5%; Pred. No. 1.4e-66;
 Matches 151; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 60
 |||||
 Db 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 87
 |||||

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 |||||
 Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHMDKAIKSLRSITLLRALGAQ-EAIS 146
 |||||

QY 121 PDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165
 |||||
 Db 147 LPDAASAAPLRTITADTFCKFLFRVYSNLFRLGKLYTGEACRRGD 191
 |||||

RESULT 3
 I84613
 erythropoietin precursor - rhesus macaque

C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: I84613
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence hom
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I84613
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-192 <RES>
 A:Cross-references: GB:I10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-192/Product: erythropoietin #status predicted <MAT>
 F:34-187,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 89.8%; Score 759.5; DB 1; Length 192;
 Best Local Similarity 90.3%; Pred. No. 4.3e-66;
 Matches 149; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 60
 |||||
 Db 28 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 87
 |||||

QY 61 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHVDKAVSGLSRLTLLRALGAQKEAIS 120
 |||||
 Db 88 VEVWQGLALLSEAVLRGQALLVNSQPWEPLQLHMDKAIKSLRSITLLRALGAQ-EAIS 146
 |||||

QY 121 PDAASAAPLRTITADTFKFLFRVYSNLFRLGKLYTGEACRTGD 165
 |||||
 Db 147 LPDAASAAPLRTITADTFCKFLFRVYSNLFRLGKLYTGEACRRGD 191
 |||||

RESULT 4
 I46083
 erythropoietin precursor - cat (fragment)
 C:Species: Felis silvestris catus (domestic cat)
 C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: I46083
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence hom
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46083
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-188 <WEN>
 A:Cross-references: GB:I10606; NID:gl63820; PIDN:AAA30807.1; PID:gl63821
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F:23-188/Product: erythropoietin #status predicted <MAT>
 F:29-183,51-55/Disulfide bonds: #status predicted
 F:46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:148/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.3%; Score 713; DB 1; Length 188;
 Best Local Similarity 84.2%; Pred. No. 1.3e-61;
 Matches 139; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 60
 |||||
 Db 23 APPRLICDSRVLYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFKYAKRMEVGQQA 82
 |||||

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALLGAQKEAIS 120
 |||||
 DB 83 VEVWQGLALLSEAVLRGQALLVNSSQPSETQLHVDKAVSGLRSLTLLRALLGAQKEAIS 142
 |||||
 QY 121 PPDAASAAPLRTITADTKFLFRVYSNPLRGKLLKLYTGEACRTGD 165
 |||||
 DB 143 LPEATSAAPLRTITADTKFLFRVYSNPLRGKLLKLYTGEACRTGD 187
 |||||

RESULT 5

S28148
 erythropoietin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 21-Jul-2000
 C:Accession: S28148; I62743
 R:Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
 Biochim. Biophys. Acta 1171, 99-102, 1992
 A:Title: Nucleotide sequence of rat erythropoietin.
 A:Reference number: S28148; MUID:93042015; PMID:1420369
 A:Accession: S28148
 A:Molecule type: mRNA
 A:Residues: 1-192 <NAG>
 A:Cross-references: GB:D10763; NID:g220735; PIDN:BA01593.1; PID:g220736
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I62743
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-192 <RES>
 A:Cross-references: GB:L10608; NID:g204060; PIDN:AAA41126.1; PID:g204061
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of

C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-192/Product: erythropoietin #status predicted <MAT>
 F:33-187,55-165/Disulfide bonds: #status predicted
 F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.9%; Score 701; DB 1; Length 192;
 - Best Local Similarity 82.4%; Pred. No. 2e-60;
 Matches 136; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLLYLLAKEAENITTCACAEHCSSLNENITVPDTKVNFWAKRMEVQQA 60
 |||||
 DB 27 APPRLICDSRVLYRLLYLLAKEAENITTCACAEHCSSLNENITVPDTKVNFWAKRMEVQQA 86
 |||||
 QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALLGAQKEAIS 120
 |||||
 DB 87 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALLGAQKEAIS 146
 |||||
 QY 121 PPDAASAAPLRTITADTKFLFRVYSNPLRGKLLKLYTGEACRTGD 165
 |||||
 DB 147 PPDAASAAPLRTITADTKFLFRVYSNPLRGKLLKLYTGEACRTGD 191
 |||||

RESULT 6

I46401
 erythropoietin precursor - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: I46401; I47077
 R:Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
 Mol. Cell. Endocrinol. 93, 107-116, 1993
 A:Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pl
 A:Reference number: I46401; MUID:93351736; PMID:8349021
 A:Accession: I46401
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-194 <FUX>
 A:Cross-references: EMBL:224681; NID:g395049; PIDN:CAA80848.1; PID:g395050
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence hom
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I47077
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 4-15, 'L', '17-107, 'P', '109-194 <WEN>
 A:Cross-references: GB:L10610; NID:g165876; PIDN:AAA31518.1; PID:g165877
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
 C:Function:

A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-194/Product: erythropoietin #status predicted <MAT>
 F:34-189,56-60/Disulfide bonds: #status predicted
 F:51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:154/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 81.0%; Score 685.5; DB 1; Length 194;
 - Best Local Similarity 81.9%; Pred. No. 6.3e-59;
 Matches 136; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 APPRLICDSRVLYRLLYLLAKEAENITTCACAEHCSSLNENITVPDTKVNFWAKRMEVQQA 60
 |||||

DB 28 APPRLICDSRVLYRLLYLLAKEAENITTCACAEHCSSLNENITVPDTKVNFWAKRMEVQQA 87
 |||||

QY 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALLGAQKEAIS 120
 |||||

DB 88 LEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALLGAQKEAIS 147
 |||||

QY 121 PPDAASAAPLRTITADTKFLFRVYSNPLRGKLLKLYTGEACRTGD 165
 |||||

DB 148 LPDAPSAAPLRTITADTKFLFRVYSNPLRGKLLKLYTGEACRTGD 193
 |||||

erythropoietin precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 22-Jun-1999
 C:Accession: A24902; A24901

R:Shoenmaker, C.B.; Mitsock, L.D.
 Mol. Cell. Biol. 6, 849-858, 1986
 A:Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
 A:Reference number: A24902; MUID:87039105; PMID:3773894
 A:Accession: A24902

A:Molecule type: DNA
 A:Residues: 1-192 <SHO>
 A:Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 4

R:McDonald, J.D.; Lin, F.K.; Goldwasser, E.
 Mol. Cell. Biol. 6, 842-848, 1986
 A:Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin g
 A:Reference number: A24901; MUID:87039104; PMID:3022133
 A:Accession: A24901

A:Molecule type: DNA
 A:Residues: 1-67, 'P', '69-192 <MCD>
 A:Cross-references: GB:M12930; NID:g193086; PIDN:AAA37570.1; PID:g387152
 C:Comment: Erythropoietin is produced by kidney or liver of adult mammals and by live
 C:Genetics:

A:Introns: 5/1; 52/3; 81/3; 141/3
 C:Function:
 A:Description: the primary inducer of erythrocyte formation
 C:Superfamily: erythropoietin
 C:Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-192/Product: erythropoietin #status predicted <MAT>
 F:33-187,55-165/Disulfide bonds: #status predicted
 F:50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.5%; Score 681; DB 1; Length 192;
 Best Local Similarity 79.4%; Pred. No. 1.7e-58;
 Matches 131; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGOQA 60
 DB 27 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGOQA 86
 QY 61 VEWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 DB 87 IEVWQGLSLLSEAILQAALLANSOPPTELQHLIDKALISGLRSLTLLRLVLSGAKELMS 146
 QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
 DB 147 PPDTPPAPLRTITVDFCKLFRVYANFLRGKLYTGEVCRGD 191

RESULT 8
 JC7699
 erythropoietin - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
 C:Accession: JC7699
 R:Villalta, A.; Wu, D.; Margalith, M.; Hobart, P.
 Biochem. Biophys. Res. Commun. 284, 823-827, 2001
 A:Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injection
 A:Reference number: JC7699; MUID:21290682; PMID:11396976
 A:Contents: Kidney
 A:Accession: JC7699
 A:Molecule type: DNA
 A:Residues: 1-195 <VIL>
 A:Cross-references: GB:AF290943
 C:Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
 cytes.

C:Genetics:
 A:Gene: epo
 C:Superfamily: erythropoietin
 C:Keywords: glycoprotein; kidney

Query Match 80.4%; Score 680.5; DB 2; Length 195;
 Best Local Similarity 81.3%; Pred. No. 1.9e-58;
 Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGOQA 60
 DB 29 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNPHYHKKSEAGRHA 88
 QY 61 VEWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 DB 89 VEWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGVQKEAVS 148
 QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
 DB 149 PPEAASAAPLRTITVADTCLKLFRIYSNLFRLGKLYTGEACRGD 194

RESULT 9
 I46578
 erythropoietin - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: I46578
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46578
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-190 <WEN>
 A:Cross-references: GB:L10607; NID:gl164445; PIDN:AAA31029.1; PID:gl164446
 C:Superfamily: erythropoietin

Query Match 80.1%; Score 678; DB 2; Length 190;
 Best Local Similarity 82.0%; Pred. No. 3.3e-58;
 Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGOQA 60
 DB 23 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGOQA 82
 QY 61 VEWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 DB 83 MEVWQGLALLSEAILQOALLANSQPSEALQHLVDKAVSGLRSLTLLRALGAQKEAIP 142
 QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGKLYTGEACRTGD 165
 DB 143 LPDASPSSAPLRTITFAVDTLCKLFRNYSNLFRLGKLYTGEACRRD 189

RESULT 10
 I46199
 erythropoietin - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
 C:Accession: I46199
 R:Wen, D.; Boissel, J.
 Blood 82, 1507-1516, 1993
 A:Title: Erythropoietin structure-function relationships: High degree of sequence homology
 A:Reference number: I46083; MUID:93372347; PMID:8364201
 A:Accession: I46199
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-175 <WEN>
 A:Cross-references: GB:L13027; NID:g290087; PIDN:AAA30842.1; PID:g552347
 C:Superfamily: erythropoietin

Query Match 75.4%; Score 638; DB 2; Length 175;
 Best Local Similarity 81.0%; Pred. No. 2.2e-54;
 Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGOQA 60
 DB 23 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFTYTKRMDVGOQA 82
 QY 61 VEWQGLALLSEAVLRQALLVNSSQPWEPLQHLVDKAVSGLRSLTLLRALGAQKEAIS 120
 DB 83 LEVWQGLALLSEAILRQALLANASQPSETPQLHVDKAVSSLSRSLTLLRALGAQKEAMS 142
 QY 121 PPDAASAAPLRTITADTFKRLFRVYSNLFRLGK 153
 DB 143 LPEASAPLRTITVDTLCKLFRVYSNLFRLGK 175

RESULT 11
 G02729
 thrombopoietin - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C:Accession: G02729
 R:Im, S.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: H01637
 A:Accession: G02729
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-353 <IMX>
 A:Cross-references: EMBL:U59493; NID:gl1401245; PIDN:AAB03392.1; PID:gl1401246
 C:Genetics:
 A:Gene: htpo

Query Match 10.6%; Score 90; DB 2; Length 353;
 Best Local Similarity 26.3%; Pred. No. 0.6;
 Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;

QY 1 APRRLICDSRVRLRYLLEAKEAENITTCGAHCSSLNENITVPDTKVNFYANKRMEVGOQA 60

```

Db      24 APP--ACDLRVLSKLLRDSHVLHSLKSKQCPEVHPLPTPVLLPAVDFSLGKWTQMEETKA 81
      61 VEVWQGLALLSEAVL--RGQALLVNSQPWEPLQLHVDKAVSGLRSITLTLLRALGAQKEA 118
      82 QDILGAVTLLLEGVMAARGQLPTCLSLGLGQLSEQVRLLLGALQSL-----LGTQ--- 132
      119 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGK 154
      133 -LPOG-----RTTAHKDPNAIFLSFOHLLRGKVR 161

RESULT 12
180105
N:thrombopoietin precursor - human
C:Species: Homo sapiens (man)
C:Alternate names: c-MPL ligand; megakaryocyte growth and development factor precursor
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 20-Jun-2000
C:Accession: I59281; I80105; S45331; S48740; I38672; I52610
R:Poster, D.C.; Sprecher, C.A.; Grant, F.J.; Kramer, J.M.; Kuijper, J.L.; Holly, R.D.; W
Proc. Natl. Acad. Sci. U.S.A. 91, 13023-13027, 1994
A:Title: Human thrombopoietin: gene structure, cDNA sequence, expression, and chromosomal
A:Reference number: I59281; MUID:95108091; PMID:7809166
A:Accession: I59281
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <RE2>
A:Cross-references: GB:I36051; NID:g533214; PIDN:AAC37568.1; PID:g533215
A:Accession: I80105
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-353 <RES>
A:Cross-references: GB:I36052; NID:g533216; PIDN:AAC37566.1; PID:g533217
R:de Sauvage, F.J.; Hass, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, S.A.
Nature 369, 533-538, 1994
D.V.; Eaton, D.L.
A:Title: Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl ligand.
A:Reference number: S45331; MUID:94261202; PMID:8202154
A:Accession: S45331
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-353 <SAU>
A:Cross-references: GB:I33410; NID:g506826; PIDN:AAA59857.1; PID:g506827
R:Sohna, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
FEBS Lett. 353, 57-61, 1994
A:Title: Molecular cloning and chromosomal localization of the human thrombopoietin gene
A:Reference number: S48740; MUID:95010765; PMID:7926023
A:Accession: S48740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <SOH>
A:Cross-references: GB:D32046; NID:g577319; PIDN:BAA06807.1; PID:g577320
R:Bartley, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.;
Cell 77, 1117-1124, 1994
A:Title: Identification and cloning of a megakaryocyte growth and development factor tha
A:Reference number: A54463; MUID:94291201; PMID:8020099
A:Accession: I38672
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112,'E',114-353 <RES>
A:Cross-references: EMBL:U11025; NID:g511223; PIDN:AAA50553.1; PID:g558078
R:Gurney, A.L.; Kuang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
Blood 85, 981-988, 1995
A:Title: Genomic structure, chromosomal localization, and conserved alternative splice
A:Reference number: I52610; MUID:95152076; PMID:7849319
A:Accession: I52610
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-353 <RES4>
A:Cross-references: GB:S76771; NID:g914225; PIDN:AAB33390.1; PID:g914226
C:Genetics:
A:Gene: GDB:THPO; MGDF
A:Cross-references: GDB:374007; OMIM:600044

```

```

A:Map position: 3q26.3-3q27
A:Introns: 5/1; 47/3; 76/3; 132/3
C:Keywords: alternative splicing; cytokine; glycoprotein

Query Match      10.5%; Score 89; DB 2; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.75; Mismatches 20; Gaps 5;
Matches 41; Conservative 20; Indels 75; Indels 20; Gaps 5;

QY 1 APPRLICDSRVILERYLLEAKEAENITTCGAHCISLNENITVDTKVNIFYAKRMVEVGOQA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 APP--ACDLRVLSKLLRDSHVLHSLKSKQCPEVHPLPTPVLLPAVDFSLGKWTQMEETKA 81

QY 61 VEVWQGLALLSEAVL--RGQALLVNSQPWEPLQLHVDKAVSGLRSITLTLLRALGAQKEA 118
    :: : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 QDILGAVTLLLEGVMAARGQLPTCLSLGLGQLSEQVRLLLGALQSL-----LGTQ--- 132

QY 119 ISPPDAASAAPLRTITADTFKRLFRVYSNFLRGK 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 -LPOG-----RTTAHKDPNAIFLSFOHLLRGKVR 161

RESULT 13
AB0323
ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Yersinia p
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AB0323
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92889.1; PID:g15980631; GSPDB:GN00175
C:Genetics:
A:Gene: nrdF
C:Superfamily: ribonucleoside-diphosphate reductase beta
C:Keywords: oxidoreductase

Query Match      10.4%; Score 88; DB 2; Length 323;
Best Local Similarity 25.2%; Pred. No. 0.84;
Matches 34; Conservative 20; Mismatches 59; Indels 22; Gaps 5;

QY 38 NITVPDTKYNFYAKRMVEVGOQAVEWQGLALLSEAVLRGOALLVNSSQPWEPLQLHVD- 96
    | : | | : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 2 NVVKPITRISAINWKNIE--DKDLEVN--RUTSNFWLPEKVPPLSNDIPSWATLTPHEQQ 58

QY 97 ---KAVSGLRSITLTLLRALGAQ---KEATSPDPAASAAPLRTITADTFKRLFRVYSNFLR 150
    : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 59 LIRVFTGLTLDTQNTLGAPALIKDAITPHEEAIFSNISPFMEAVHARSYSSIFSTL-- 116

QY 151 GKLLKLTGCACTGD 165
    | | |
Db 117 -----CLTSD 121

RESULT 14
AE0959
Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica sero
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0959
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerthon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

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Search completed: June 13, 2003, 15:04:42
Job time : 33 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:03:00 ; Search time 12 seconds
(without alignments)
570.300 Million cell updates/sec

Title: US-09-830-964-1
Perfect score: 846
Sequence: 1 APPRLICDSRLVRLRYLEAK.....SNELRGKLYTGEACRTGD 165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	846	100.0	193	1	EPO_HUMAN	P01588	homo sapien
2	764.5	80.4	192	1	EPO_HUMAN	P07865	macaca fasc
3	759.5	89.8	192	1	EPO_HUMAN	Q28513	macaca mula
4	706	83.5	192	1	EPO_FELCA	P33708	felis silve
5	701	82.9	192	1	EPO_RAT	P29676	rattus norv
6	692.5	81.9	192	1	EPO_BOVIN	P48617	bos taurus
7	689	81.4	192	1	EPO_MOUSE	P07321	mus musculu
8	685.5	81.0	194	1	EPO_SHEEP	P33709	ovis aries
9	678	80.1	190	1	EPO_PIG	P49157	sus scrofa
10	638	75.4	175	1	EPO_CANFA	P33707	canis famil
11	109	12.9	352	1	TPO_CANFA	P42705	canis famil
12	89	10.5	353	1	TPO_HUMAN	P40225	homo sapien
13	80.5	9.5	3033	1	POLG_HCVJ78	P26661	h genome po
14	78.5	9.3	897	1	EP15_MOUSE	P42567	mus musculu
15	78	9.2	747	1	ATCS_SYN7	P37279	synechococc
16	77	9.1	548	1	CH60_BUCAP	O51832	buchnera ap
17	76.5	9.0	386	1	CTBP_DRONE	O46036	drosophila
18	76	9.0	551	1	CH60_BUCAP	O59177	buchnera ap
19	74.5	8.8	552	1	CH60_PSEST	O33500	pseudomonas
20	74.5	8.8	809	1	HRPB_ECOLI	P37024	escherichia
21	74	8.7	326	1	TPO_RAT	P49745	rattus norv
22	74	8.7	1564	1	PDRA_YEAST	P51533	saccharomyc
23	73.5	8.7	830	1	GCL2_MOUSE	Q9jhd2	mus musculu
24	73.5	8.7	837	1	GCL2_HUMAN	Q92830	homo sapien
25	73	8.6	263	1	YH25_DEIRA	O83030	dainococcus
26	73	8.6	1089	1	IMB3_YEAST	P32337	saccharomyc
27	72.5	8.6	762	1	SLAP_ACEKI	P22258	acetogenium
28	72	8.5	356	1	TPO_MOUSE	P40226	mus musculu
29	72	8.5	548	1	CH60_BUCAI	P25750	buchnera ap
30	70.5	8.3	217	1	YH2D_ECOLI	P76909	escherichia
31	70.5	8.3	381	1	MODD_MYCAV	Q48919	mycobacteri
32	70.5	8.3	543	1	CH60_BARBA	P35635	bartonella
33	70.5	8.3	896	1	EP15_HUMAN	P42566	homo sapien

RESULT 1

ID	EPO_HUMAN	STANDARD;	PRT;	193 AA.
AC	P01588; Q9UHA0; Q9UEZ5; Q9UDZ0;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Erythropoietin precursor (Epoetin).			
GN	EPO.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]	SEQUENCE FROM N.A.			
RP	MEDLINE=85137899; PubMed=3838366;			
RX	Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.,			
RA	Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,			
RA	Kawakita M., Shimizu T., Miyake T.;			
RA	"Isolation and characterization of genomic and cDNA clones of human			
RT	erythropoietin.";			
RL	Nature 313:806-810(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067948; PubMed=3865178;			
RA	Lin F.-K., Sugus S., Lin C.-H., Browne J.K., Smalling R., Egrle J.C.,			
RA	Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai P.-H.,			
RA	Goldwasser E.;			
RT	"Cloning and expression of the human erythropoietin gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).			
[3]	SEQUENCE FROM N.A.			
RP	MEDLINE=99018118; PubMed=9799793;			
RX	Gloekner G., Scherer S., Schattevoy R., Boright A., Weber J.,			
RA	Tsui L.-C., Rosenthal A.;			
RT	"Large-scale sequencing of two regions in human chromosome 7q22:			
RT	analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci			
RT	reveals 17 genes.";			
RL	Genome Res. 8:1060-1073(1998).			
[4]	SEQUENCE FROM N.A.			
RP	Rupert J.L., Hochachka P.W.;			
RT	"Erythropoietin gene sequence in the Quechua, a high altitude native			
RT	population.";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
[5]	SEQUENCE OF 58-193 FROM N.A. AND VARIANTS HEPATOCELLULAR CARCINOMA.			
RP	MEDLINE=93384593; PubMed=8396923;			
RA	Funakoshi A., Muta H., Baba T., Shimizu S.;			
RT	"Gene expression of mutant erythropoietin in hepatocellular			
RT	carcinoma.";			
RL	Biochem. Biophys. Res. Commun. 195:717-722(1993).			
[6]	SEQUENCE OF 28-193, AND DISULFIDE BONDS.			
RP	TISSUE=Urine;			
RC	MEDLINE=86140080; PubMed=3949763;			
RX				

34	70	8.3	319	1	RIR4_SALTY	P17424	salmonella
35	70	8.3	547	1	CH60_LEGPN	P26878	legionella
36	69.5	8.2	907	1	GACS_PSESV	P48027	pseudomonas
37	69.5	8.2	1327	1	TNKL_HUMAN	O95271	homo sapien
38	69	8.2	353	1	NADA_YERPE	Q89y8	yersinia pe
39	69	8.2	544	1	CH60_FRATU	P94798	francisella
40	69	8.2	552	1	CH60_COXBU	P19421	coxlella bu
41	69	8.2	1128	1	DNBI_HSVSA	P24910	herpesvirus
42	68.5	8.1	360	1	CYS2_WAIZE	Q10717	zea mays (m
43	68.5	8.1	418	1	CUN2_TREIRE	P07982	trichoderma
44	68.5	8.1	778	1	RGL2_MOUSE	Q61193	mus musculu
45	68	8.0	366	1	QUEA_SYNY3	Q55850	synechocyst

ALIGNMENTS

RA Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.:
 RT "Structural characterization of human erythropoietin."
 RL J. Biol. Chem. 261:3116-3121(1986).
 RN [7]
 RP PRELIMINARY SEQUENCE OF 28-57.
 RX MEDLINE=84135751; PubMed=6698989;
 RA Yanagawa S., Hirade K., Ohnata H., Sasaki R., Chiba H., Ueda M.,
 RA Goto M.;
 RT "Isolation of human erythropoietin with monoclonal antibodies."
 RL J. Biol. Chem. 259:2707-2710(1984).
 RN [8]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=88153657; PubMed=3346214;
 RA Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
 RA Kobata A.;
 RT "Comparative study of the asparagine-linked sugar chains of human
 RT erythropoietins purified from urine and the culture medium of
 RT recombinant Chinese hamster ovary cells."
 RL J. Biol. Chem. 263:3657-3663(1988).
 RN [9]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=89118279; PubMed=3219367;
 RA Sasaki H., Ochi N., Dell A., Fukuda M.;
 RT "Site-specific glycosylation of human recombinant erythropoietin:
 RT analysis of glycopeptides or peptides at each glycosylation site by
 RT fast atom bombardment mass spectrometry."
 RL Biochemistry 27:8618-8626(1988).
 RN [10]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=92314463; PubMed=1820196;
 RA Takeuchi M., Kobata A.;
 RT "Structures and functional roles of the sugar chains of human
 RT erythropoietins."
 RL Glycobiology 1:337-346(1991).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=98445092; PubMed=9774108;
 RA Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
 RA Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
 RA Elliott S., Stiney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
 RA Egnie J., Stroud R.M.;
 RT "Efficiency of signalling through cytokine receptors depends
 RT critically on receptor orientation."
 RL Nature 395:511-516(1998).
 CC [1]
 CC FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC [2]
 CC SUBCELLULAR LOCATION: Secreted.
 CC [3]
 CC TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC [4]
 CC PHARMACEUTICAL: Used for the treatment of anemia. Available under
 CC the names Epogen (Amgen), Epogin (Chugai), Epomax (Elanex), Eprex
 CC (Janssen-Cilag), NeoRecormon or Recormon (Roche), and Procrit
 CC (Ortho Biotech). Variations in the glycosylation pattern of EPO
 CC distinguishes these products. Epogen, Epogin, Eprex and Procrit
 CC are generically known as epoetin alfa, NeoRecormon and Recormon as
 CC epoetin beta and Epomax as epoetin omega.
 CC [5]
 CC SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
 CC [6]
 CC DATABASE: NAME=Rad Systems' cytokine source book: EPO;
 CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=197".
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 CC -----
 CC EMBL; X02158; CAA26095.1; -
 CC EMBL; X02157; CAA26094.1; -
 CC EMBL; M11319; AAA52400.1; -
 CC EMBL; AF053356; AAC78791.1; -

DR EMBL; AF202308; AAF23132.1; -
 DR EMBL; AF202306; AAF23132.1; JOINED.
 DR EMBL; AF202307; AAF23132.1; JOINED.
 DR EMBL; AF202310; AAF23133.1; -
 DR EMBL; AF202309; AAF23133.1; JOINED.
 DR EMBL; AF202311; AAF17572.1; -
 DR EMBL; AF202314; AAF23134.1; -
 DR EMBL; AF202312; AAF23134.1; JOINED.
 DR EMBL; AF202313; AAF23134.1; JOINED.
 DR EMBL; S65458; AAD13964.1; -
 DR PIR; A01855; ZUHU.
 DR PIR; A25384; A25384.
 DR PIR; A24744; A24744.
 DR PIR; A22210; A22210.
 DR PDB; 1EER; 01-OCT-99.
 DR PDB; 1CN4; 11-AUG-99.
 DR GlycoSuiteDB; P01588; -
 DR Genew; HGNC:3415; EPO.
 DR MIN; 133170; -
 DR InterPro; IPR001323; EPO_TPO.
 DR InterPro; IPR003013; Erythroptn.
 DR Pfam; PF00758; EPO_TPO; 1
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal; Pharmaceutical;
 KW 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 193 ERYTHROPOIETIN.
 FT PROPEP 190 193 MAY BE REMOVED IN PROCESSED PROTEIN.
 FT DISULFID 34 188
 FT DISULFID 56 60
 FT CARBOHYD 51 51 N-LINKED (GLCNAC...).
 FT CARBOHYD 65 65 /FTID=CAR_000052.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC...).
 FT CARBOHYD 153 153 /FTID=CAR_000166.
 FT VARIANT 131 132 N-LINKED (GLCNAC...).
 FT VARIANT 149 149 SL -> NF (IN AN HEPATOCELLULAR
 FT VARIANT 149 149 /FTID=VAR_009870.
 FT CONFLICT 40 40 P -> Q (IN AN HEPATOCELLULAR CARCINOMA).
 FT CONFLICT 85 85 E -> Q (IN REF. 1; CAA26095).
 FT CONFLICT 140 140 Q -> QQ (IN REF. 5).
 FT CONFLICT 140 140 G -> R (IN REF. 1; CAA26095).
 SQ SEQUENCE 193 AA; 21306 MW; C91F0E4C26A52033 CRC64;
 Query Match 100.0%; Score 846; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.9e-76;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APRRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKYNFVAKRMVGGQA 60
 DB 28 APRRLICDSRVLYRLLEAKEAENITTCGAHCNENITVPDTKYNFVAKRMVGGQA 87
 QY 61 VEVWQGLALLSEAVLRQALLVNSQWPEPQLQHVDAKAVSGLRSLTTLRALCAQKEATS 120
 DB 88 VEVWQGLALLSEAVLRQALLVNSQWPEPQLQHVDAKAVSGLRSLTTLRALCAQKEATS 147
 QY 121 PPDAASAAPLRTTADTFKRLFRVSNFLRGKLYTGACRTGD 165
 DB 148 PPDAASAAPLRTTADTFKRLFRVSNFLRGKLYTGACRTGD 192
 RESULT 2
 EPO_MACFA
 ID EPO_MACFA STANDARD; PRT; 192 AA.
 AC P07865;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.


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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBJ_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Goodman R.E., Bell R.G.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 5-192 FROM N.A.
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
CC -!- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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DR EMBL; U00685; AAA18282.1; -
DR EMBL; L10606; AAA30807.1; -
DR HSSP; P01588; ICN4.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 192 ERYTHROPOIETIN.
FT DISULFID 33 187 BY SIMILARITY.
FT FT 55 59 BY SIMILARITY.
FT FT 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 44 44 G -> E (IN REF. 2).
SQ SEQUENCE 192 AA; 20914 MW; 61C5EA0F5E937293 CRC64;

Query Match 83.5%; Score 706; DB 1; Length 192;
Best Local Similarity 83.6%; Pred. No. 1.3e-62;
Matches 138; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLYLEAKEAENITTCGAHCNSINENITVPDTKVFYANKRMVEGQQA 60
Db 27 APPRLICDSRVLYRLYLEAKEAENITTCGAHCNSINENITVPDTKVFYANKRMVEGQQA 86
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHLVDKAVSGLSRLTLLRALGAQKEAIS 120
Db 87 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHLVDKAVSGLSRLTLLRALGAQKEAIS 146
QY 121 PPDAASAAPLTITADTFKFLRYVSNFLRCKLKLTYGACRTGD 165
Db 147 LPEATSAAPLTFTVDTKFLRYVSNFLRCKLKLTYGACRTGD 191

EPO_RAT
ID EPO_RAT STANDARD; PRT; 192 AA.
AC P29676; p70504;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBJ_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=93042015; PubMed=1420369;
RA Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura K.,
RA Sasaki R.;
RT "Nucleotide sequence of rat erythropoietin.";
RL Biochim. Biophys. Acta 1171:99-102(1992).
RN [2]
RP SEQUENCE OF 4-192 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
RA Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -!- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
CC -!- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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DR EMBL; D10763; BAA01593.1; -
DR EMBL; L10608; AAA41126.1; -
DR PIR; S28148; S28148.
DR HSSP; P01588; ICN4.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 192 ERYTHROPOIETIN.
FT DISULFID 33 187 BY SIMILARITY.
FT FT 55 59 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ SEQUENCE 192 AA; 21286 MW; 3EA632737E7D2443 CRC64;

Query Match 82.9%; Score 701; DB 1; Length 192;
Best Local Similarity 82.4%; Pred. No. 4e-62;
Matches 136; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APPRLICDSRVLYRLYLEAKEAENITTCGAHCNSINENITVPDTKVFYANKRMVEGQQA 60
Db 27 APPRLICDSRVLYRLYLEAKEAENITTCGAHCNSINENITVPDTKVFYANKRMVEGQQA 86
QY 61 VEVWQGLALLSEAVLRQALLVNSQPWEPLQHLVDKAVSGLSRLTLLRALGAQKEAIS 120

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Db 87 VEVWQGLSLSEALQALQANSSQPPELQHLIDKATISGLRSLTLLRVLGAQKELMS 146
 QY 121 PPDAAAPLRTITADTFRKLFVYSNLFGRKLYTGEACRTGD 165
 DB 147 PPDATQAPLRTITADTFRKLFVYSNLFGRKLYTGEACRRGD 191

RESULT 6

EPO_BOVIN STANDARD; PRT; 192 AA.
 AC P48617:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Boran; TISSUE=Kidney;
 RX MEDLINE=96257233; PubMed=8666286;
 RA Suliman H.B., Majlwa P.A.O., Feldman B.F., Mertens B.,
 RA Logan-Henfrey L.L.;
 RT "Cloning of a cDNA encoding bovine erythropoietin and analysis of its
 RT transcription in selected tissues.";
 RL Gene 171:275-280(1996).
 CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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 CC
 DR EMBL; U41354; AAB41268.1; -;
 DR EMBL; U44762; AAB86653.1; -;
 DR HSP; P01588; ICM4.
 DR InterPro; IPR001323; EPO_TPO.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PRINTS; PR00272; ERYTHROPTN.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 192 ERYTHROPOIETIN.
 FT DISULFID 32 187 BY SIMILARITY.
 FT DISULFID 54 58 BY SIMILARITY.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 63 63 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 108 108 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 192 AA; 21075 MW; DBC419022F7B483A CRC64;

Query Match

Best Local Similarity 81.98; Score 692.5; DB 1; Length 192;

Matches 138; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 1 APRILCDSRVLYRLLLEAKEAENITTCGAHCSNENITVPDTKYNFVAKRMEVQQA 60
 DB 26 APARLICDSRVLYRLLLEAKEAENATMGCAEGCSFNENITVPDTKYNFVAKRMEVQQA 85
 QY 61 VEVWQGLSLSEALVLRGALLVNSQPPELQHLIDKATISGLRSLTLLRVLGAQKEAIS 120

Db 86 LEVWQGLSLSEAILRGOALLANASQPCEALRLHVDKAVSGRLSLTLLRVLGAQKEAIS 145
 QY 121 PPDAA-SAAPLRTITADTFRKLFVYSNLFGRKLYTGEACRTGD 165
 DB 146 LPDAPSAAPLRAFTVDALSKLFRISNLFGRKLYTGEACRRGD 191

RESULT 7

EPO_MOUSE STANDARD; PRT; 192 AA.
 AC P07321:
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor.
 GN EPO.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039105; PubMed=3773894;
 RA Shoemaker C.B., Mitsock L.D.;
 RT "Murine erythropoietin gene: cloning, expression, and human gene
 RT homology.";
 RL Mol. Cell. Biol. 6:849-858(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87039104; PubMed=3022133;
 RA McDonald J.D., Lin F.-K., Goldwasser E.;
 RT "Cloning, sequencing, and evolutionary analysis of the mouse
 RT erythropoietin gene.";
 RL Mol. Cell. Biol. 6:842-848(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFP2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 RN [4]
 RP SEQUENCE OF 1-52 FROM N.A.
 RC STRAIN=ICFW;
 RX MEDLINE=98030528; PubMed=9365246;
 RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
 RA Lacombe C.;
 RT "Abnormal erythropoietin (Epo) gene expression in the murine
 RT erythroleukemia IW32 cells results from a rearrangement between the
 RT G-protein beta2 subunit gene and the Epo gene.";
 RL Oncogene 15:1995-1999(1997).
 CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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 CC
 DR EMBL; M12482; AAA37568.1; -;
 DR EMBL; M12930; AAA37570.1; -;

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DR EMBL; AF312033; AAK28825.1; -.
DR EMBL; Y11971; CAA72707.1; -.
DR PIR; A24901; A24901.
DR PIR; A24902; A24902.
DR HSSP; P01588; 1CN4.
DR MGD; MGI:95407; Epo.
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 26
FT CHAIN 27 192 ERYTHROPOIETIN.
FT DISULFID 33 187 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ SEQUENCE 192 AA; 21365 MW; 65F94E214E0DEF2E CRC64;

Query Match 81.4%; Score 689; DB 1; Length 192;
Best Local Similarity 80.0%; Pred. No. 6.2e-61;
Matches 132; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 APPRLCDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAKRMVEVCQA 60
Dd 27 APPRLCDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAKRMVEVCQA 86
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGRLSRLTLLRALGAKQKALS 120
Dd 87 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGRLSRLTLLRALGAKQKALS 146
QY 121 PDPAASAPLRTITADTFKRLFRVYSNLFRLGKLYTGACRTGD 165
Dd 147 PPDTPPPAPLRLTVDTECKLFRVYANFLRGKLYTGACRRGD 191

RESULT 8
EPO_SHEEP
ID EPO_SHEEP STANDARD; PRT; 194 AA.
AC F33709; Q28572;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor.
GN EPO.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93351736; PubMed=8349021;
RA Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.;
RT "The sheep erythropoietin gene: molecular cloning and effect of
RT hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
RT adult sheep.";
RL Mol. Cell. Endocrinol. 93:107-116(1993).
RN [2]
RP SEQUENCE OF 4-194 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
CC -1- SUBCELLULAR LOCATION: Secreted.

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CC -1- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
AND BY LIVER OF FETAL OR NEONATAL MAMMALS.

CC -1- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.

CC -----

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CC -----

CC EMBL; Z24681; CAA80848.1; -.
CC EMBL; L10610; AAA31518.1; -.
CC HSSP; P01588; 1CN4.
CC InterPro; IPR001323; EPO_TPO.
CC InterPro; IPR003013; Erythroptn.
CC Pfam; PF00758; EPO_TPO; 1.
CC PRINTS; PR00272; ERYTHROPTN.
CC PROSITE; PS00817; EPO_TPO; 1.
KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
FT SIGNAL 1 27
FT CHAIN 28 194 ERYTHROPOIETIN.
FT DISULFID 34 189 BY SIMILARITY.
FT DISULFID 56 60 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 16 16 F -> L (IN REF. 2).
FT CONFLICT 108 108 L -> P (IN REF. 2).
SQ SEQUENCE 194 AA; 21335 MW; C025AAB0528131A9 CRC64;

Query Match 81.0%; Score 685.5; DB 1; Length 194;
Best Local Similarity 81.9%; Pred. No. 1.4e-60;
Matches 136; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

QY 1 APPRLCDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAKRMVEVCQA 60
Dd 28 APPRLCDSRVLELYLLEAKEAENITTCGAHCNSLNENITVPDTKVNFAKRMVEVCQA 87
QY 61 VEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGRLSRLTLLRALGAKQKALS 120
Dd 88 LEVWQGLALLSEAVLRGQALLVNSQWPPELQHLVDKAVSGRLSRLTLLRALGAKQKALS 147
QY 121 PDPAASAPLRTITADTFKRLFRVYSNLFRLGKLYTGACRTGD 165
Dd 148 LPDAPASAPLRTITADTFKRLFRVYSNLFRLGKLYTGACRRGD 193

RESULT 9
EPO_PIG
ID EPO_PIG STANDARD; PRT; 190 AA.
AC P49157;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythropoietin precursor (Fragment).
GN EPO.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93372347; PubMed=8364201;
RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
RA Czelusniak J., Goodman M., Bunn H.F.;
RT "Erythropoietin structure-function relationships: high degree of
RT sequence homology among mammals.";
RL Blood 82:1507-1516(1993).
CC -1- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A

CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -!- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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 CC -----

DR EMBL; L10607; AAA31029.1; -
 DR HSSP; P01588; 1CN4.
 DR InterPro: IPR001323; EPO_TPO.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 190 ERYTHROPOIETIN.
 FT DISULFID 29 185 BY SIMILARITY.
 FT DISULFID 51 55 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 190 AA; 20888 MW; A75BD6CCE5077E2A CRC64;

Query Match 80.1%; Score 678; DB 1; Length 190;
 Best Local Similarity 82.0%; Pred. No. 7.5e-60;
 Matches 137; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 1 APRLLCDSRVLYRILEAKEAENITGCAEHCSLNENITVPTKYNFYAKRMVEGQQA 60
 Db 23 APRLLCDSRVLYRILEAKEAENITGCAEHCSLNENITVPTKYNFYAKRMVEGQQA 82
 QY 61 VEVWQGLALLSEALVLRQALLVNSQPWEPLQLHVDKAVSLRLTLTLRALGAQKEAIS 120
 Db 83 MEVWQGLALLSEALVLRQALLVNSQPWEPLQLHVDKAVSLRLTLTLRALGAQKEAIP 142
 QY 121 PPDA-ASAAPLRITADTKFRVYNSFLRGKLYTGEACRTGD 165
 Db 143 LPDASPSSATPLRTFAVDTLCKLFRNYSNLFRLGKLYTGEACRRRD 189

RESULT 10
 EPO_CANFA STANDARD; PRT; 175 AA.
 AC P33707;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Erythropoietin precursor (fragment).
 GN EPO.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93372347; PubMed=8364201;
 RA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
 RA Czelusniak J., Goodman M., Bunn H.F.;
 RT "Erythropoietin structure-function relationships: high degree of
 RT sequence homology among mammals.";
 RL Blood 82:1507-1516(1993).
 CC -!- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -!- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
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DR EMBL; L13027; AAA30842.1; -
 DR HSSP; P01588; 1CN4.
 DR InterPro: IPR001323; EPO_TPO.
 DR Pfam; PF00758; EPO_TPO; 1.
 DR PROSITE; PS00817; EPO_TPO; 1.
 KW Erythrocyte maturation; Glycoprotein; Hormone; Signal.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 >175 ERYTHROPOIETIN.
 FT DISULFID 29 >175 BY SIMILARITY.
 FT DISULFID 51 55 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 175 175
 SQ SEQUENCE 175 AA; 19193 MW; B504F8DE86678BF4 CRC64;

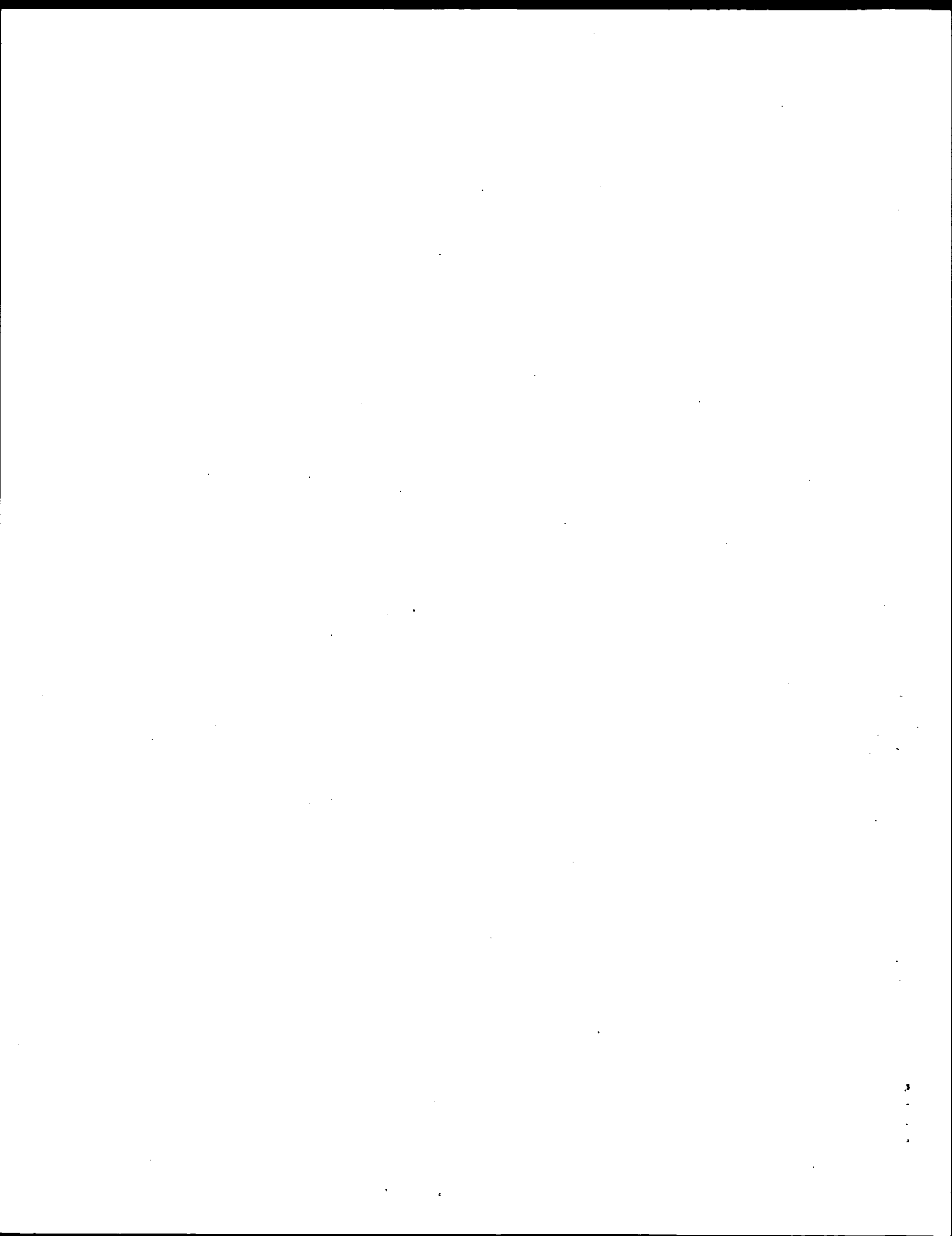
Query Match 75.4%; Score 638; DB 1; Length 175;
 Best Local Similarity 81.0%; Pred. No. 6e-56;
 Matches 124; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 APRLLCDSRVLYRILEAKEAENITGCAEHCSLNENITVPTKYNFYAKRMVEGQQA 60
 Db 23 APRLLCDSRVLYRILEAKEAENITGCAEHCSLNENITVPTKYNFYAKRMVEGQQA 82
 QY 61 VEVWQGLALLSEALVLRQALLVNSQPWEPLQLHVDKAVSLRLTLTLRALGAQKEAIS 120
 Db 83 LEVWQGLALLSEALVLRQALLVNSQPWEPLQLHVDKAVSLRLTLTLRALGAQKEAMS 142
 QY 121 PDASAAPLRITADTKFRVYNSFLRGKLYTGEACRTGD 153
 Db 143 LPDASPSSATPLRTFAVDTLCKLFRNYSNLFRLGKLYTGEACRRRD 175

RESULT 11
 TPO_CANFA STANDARD; PRT; 352 AA.
 AC P42705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin precursor (Megakaryocyte colony stimulating factor)
 DE (C-MPL ligand) (ML) (Megakaryocyte growth and development factor)
 DE (MGDF).
 GN THPO OR TPO.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-44.
 RX MEDLINE=94291201; PubMed=8020099;
 RA Bartley T.D., Bogenberger J., Hunt P., Li Y.-S., Lu H.S., Martin F.,
 RA Chang M.-S., Samal B.B., Nichol J.L., Swift S., Johnson M.J.,
 RA Hsu R.-Y., Parker V.P., Suggs S., Skrine J.D., Merewether L.A.,
 RA Clogson C., Hsu E., Hokom M.M., Hornkohl A., Choi E., Pangellinan M.,
 RA Sun Y., Mar V., McNich J., Simonet L., Jacobsen F., Xie C.,
 RA Shuttler J., Chute H., Basu R., Selander L., Trollinger D., Sieu L.,
 RA Padilla D., Trail G., Elliott G., Izumi R., Covey T., Crouse J.,
 RA Garcia A., Xu W., del Castillo J., Biron J., Cole S., Hu M.C.-T.,


```
CC 3/TRUNCATED: ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- DOMAIN: TWO-DOMAIN STRUCTURE WITH AN ERYTHROPOIETIN-LIKE N-
CC TERMINAL AND A SER/PRO/THR-RICH C-TERMINAL.
CC -I- SIMILARITY: BELONGS TO THE EPO / TPO FAMILY.
CC -I- DATABASE: NAME-Rad Systems' cytokine source book: TPO;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=225".
CC -----
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CC -----
CC EMBL: L33410; AAA59857.1; -
CC EMBL: U11025; AAA50553.1; -
CC EMBL: L36051; AAC37568.1; -
CC EMBL: L36052; AAC37566.1; -
CC EMBL: D32046; BAA06807.1; -
CC EMBL: D76771; AAB33390.1; -
CC EMBL: D32047; BAA21930.1; -
CC EMBL: U59493; AAB03392.1; -
CC EMBL: U59494; AAB03393.1; -
CC EMBL: U59495; AAB03394.1; -
CC EMBL: U17071; AAA74083.1; -
CC PIR: S45331; S45331.
CC Genew: HGNC:11795; THPO.
CC MW: 60004; -
CC InterPro: IPR001323; EPO_TPO.
CC InterPro: IPR003978; Chromopoietin.
CC Pfam: PF007758; EPO_TPO; 1.
CC PRINTS: PR01485; THROMBOPOI.
CC PROSITE: PS00817; EPO_TPO; 1.
CC Cytokine: Glycoprotein; Hormone; Signal; Alternative splicing;
CC Polymorphism.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 353 THROMBOPOIETIN.
CC DISULFID 28 172 POTENTIAL.
CC FT CARBOHYD 50 106 POTENTIAL.
CC FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT VARSPLIC 133 136 MISSING (IN ISOFORM 2).
CC FT VARSPLIC 160 198 MISSING (IN ISOFORM 3).
CC FT VARIANT 14 14 L->P (IN DBSNP:1042346).
CC FT VARIANT 116 116 /FTID=VAR_011795.
CC FT VARIANT 46 46 G->E (IN DBSNP:1126665).
CC FT VARIANT 76 76 R->K (IN REF. 8).
CC FT VARIANT 113 113 M->MSQ (IN REF. 7).
CC FT VARIANT 131 131 Q->E (IN REF. 2).
CC FT VARIANT 131 131 T->P (IN REF. 7).
CC FT VARIANT 277 277 G->E (IN REF. 8; AAB03393/AAB03394).
CC FT VARIANT 346 346 S->C (IN REF. 8; AAB03393/AAB03394).
CC SEQUENCE 353 AA; 37822 MW; F0AB5449B72E5526 CRC64;
CC -----
Query Match 10.58; Score 89; DB 1; Length 353;
Best Local Similarity 26.3%; Pred. No. 0.24;
Matches 41; Conservative 20; Mismatches 75; Indels 20; Gaps 5;
Oy 1 APRLLCDISRVLYRLLLEAEAEANITGCAEHCSLNEINIVPTKYNFVAKRMVEGQQA 60
Db 24 APP--ACDLRLVSLKLLRDSHVLSRLSQCEVPIPLPTVLLPAVDLSLGEWKTQMEETKA 81
Oy 61 VEYVQGLALLSEAVL--RGQALLVNSSQPPWEPLQLHKVAKSGLRSLTLLLRLLGAQKEA 118
Db 82 QDILGAVTLLEGVMAARGQLGPTCLSSLLGQSLGGVRLLLGALQSL-----LGTQ--- 132
Oy 119 ISPPDAASAAPLRTITADTRFKLFRVYSNFKLKLK 154
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DB 133 -LPPOG-----RTTAHKDPNAIFLSFQHLRGRKVR 161
||
||
RESULT 13
POLG_HCVJ8
ID AC P26661; STANDARD: PRT; 3033 AA.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
DE Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
DE (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
DE (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
DE (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
DE NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
DE NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
OS Hepatitis C virus (Isolate HC-J8) (HCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11115;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92230232; PubMed=1314459;
RA Okamoto H., Kurai K., Okada S.-I., Yamamoto K., Lizuka H., Tanaka T.,
RA Fukuda S., Tsuda F., Mishiro S.;
RT "Full-length sequence of a hepatitis C virus genome having poor
RT homology to reported isolates: comparative study of four distinct
RT genotypes.";
RL Virology 188:331-341(1992).
CC -I- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -I- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
CC precursor polyprotein, commonly with Asp or Glu in the P6
CC position, Cys or Thr in P1 and Ser or Ala in P1'.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC [RNA](N).
CC -I- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA.
CC -I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
CC -----
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CC -----
CC EMBL: D10988; BAA01761.1; -
CC PIR: A40250; GNWJ8.
CC HSSP: P27938; LHEI.
CC MEROPS: S29.001; -
CC MEROPS: U39.001; -
CC InterPro: IPR001410; DEAD.
CC InterPro: IPR002531; HCV_NS1.
CC InterPro: IPR002518; HCV_NS2.
CC InterPro: IPR004109; HCV_NS3.
CC InterPro: IPR000745; HCV_NS4a.
CC InterPro: IPR001490; HCV_NS4b.
CC InterPro: IPR002868; HCV_NS5a.
CC InterPro: IPR002166; HCV_RdRP.
CC InterPro: IPR002522; HCV_capsid.
CC InterPro: IPR002521; HCV_core.
CC InterPro: IPR002519; HCV_env.
CC Pfam: PF00998; HCV_RdRP; 1.
CC Pfam: PF01001; HCV_NS4b; 1.
CC Pfam: PF01006; HCV_NS4a; 1.
CC Pfam: PF01006; HCV_NS5a; 1.
```

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:04:06 ; Search time 34 Seconds

(without alignments)
999.935 Million cell updates/sec

Title: US-09-830-964-1

Perfect score: 846

Sequence: 1 APRRLICDSRVLYLEAK.....SNFLRGKLYTGEACRTGD 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	680.5	80.4	195	6 Q9GKA3	Q9gka3 oryctolagus
2	680.5	80.4	195	6 Q9GKA2	Q9gka2 oryctolagus
3	678	80.1	194	6 Q9MYN8	Q9myn8 sus scrofa
4	188	22.2	50	11 Q9QV40	Q9qv40 rattus sp.
5	88	10.4	323	16 Q8ZDC8	Q8zdc8 yersinia pe
6	87.5	10.3	346	16 Q8ZK24	Q8zkd4 salmonella
7	87.5	10.3	346	16 Q8Z2M5	Q8z2m5 salmonella
8	85	10.0	3722	2 P94873	P94873 lysobacter
9	83	9.8	296	16 Q8ZAY4	Q8zay4 yersinia pe
10	83	9.8	339	16 Q9HZM7	Q9hzm7 pseudomonas
11	82.5	9.8	3033	12 Q9DDH6	Q9ddh6 hepatitis c
12	82	9.7	815	10 Q9FK91	Q9fk91 arabidopsis
13	79.5	9.4	1829	16 Q86808	Q86808 streptomyce
14	79.5	9.4	3033	12 Q9IZA1	Q9izal hepatitis c
15	79	9.3	480	10 Q43380	Q43380 avena sativ
16	79	9.3	2364	5 Q22896	Q22896 caenorhabdi

ALIGNMENTS

RESULT 1

Q9GKA3 ID Q9GKA3 PRELIMINARY; PRT; 195 AA.
AC Q9GKA3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Erythropoietin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21290682; PubMed=11396976;
RA Vilalta A., Wu D., Margalith M., Hobart P.;
RT "Rabbit EPO Gene and cDNA: Expression of Rabbit EPO after
RT Intramuscular Injection of pDNA."
RL Biochem. Biophys. Res. Commun. 284:823-827(2001).
DR EMBL; AF290943; AAC36961.1; -;
DR HSSP; P01588; ICN4;
DR InterPro; IPR001323; EPO_TPO.
DR InterPro; IPR003013; Erythroptn.
DR Pfam; PF00758; EPO_TPO; 1.
DR PRINTS; PR00272; ERYTHROPTN.
DR PROSITE; PS00817; EPO_TPO; 1.
SQ SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;

Query Match 80.4%; Score 680.5; DB 6; Length 195;

Best Local Similarity 81.3%; Pred. No. 1.4e-60;

Matches 135; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

Qy 1 APRRLICDSRVLYLEAKEAENITTCGAHCNLENITVPTKYNFYANKRMEVGQQA 60

Db 29 APARLICDSRVLYLEAKEAENITVPTKYNFYANKRMEVGQQA 88

Qy 61 VEVWQGLALLSEAVLRGCOALLVNSSQPWEPLQHVVDKAVSGLRSLTLLRALGAKOKEATS 120

Db 89 VEVWQGLALLSEAVLRGCOALLVNSSQPWEPLQHVVDKAVSGLRSLTLLRALGAKOKEATS 148

Q9MYM8	Q9MYM8	PRELIMINARY;	PRT;	194 AA.
ID	Q9MYM8			
AC	Q9MYM8;			
Q9MYM8	Q9MYM8			
DT	01-OCT-2000	(TrEMBLrel. 15, Created)		
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)		
DE	Erythropoietin precursor.			
GN	EPO			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
NCBI_TaxID=9823;				
[1]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=NORWEGIAN LANDRACE; TISSUE=KIDNEY;			
RC	David B., Harbitz I.;			
RA	"The porcine erythropoietin gene: cDNA and genomic sequences and			
RT	expression analyses. ;			
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.			
EMBL; AJ249745; CAB96416.1;				
DR	EMBL; AJ249746; CAB96417.1;			
DR	EMBL; AJ249746; CAB96417.1;			

Query Match	9.8%	Score 83	DB 16	Length 296
Best Local Similarity	24.2%	Pred. No. 3.6		
Matches 48	Conservative 34	Mismatches 62	Indels 54	Gaps 10
QY 6	ICDSRLVRLYLLEAK-EAENITTCGAECHECSLENIT-VPDTKYNFYAWKRMVEYQQAQVEV	63		
DB 32	LCDADITKVIQLTAELNAESLTVDNA--ASLDALITMLPNS-...AVEQVLLGSDGISG	85		
QY 64	WQGLALSEAVLRQALLVNSQP-----WE-----PIQLHVDKAVSG----	101		
DB 86	W--VAQLSQAQV---VIDMSSDPERSRRLAILLAVMWELDYLDAPVSGGVKKAKQNGTLSI	140		
QY 102	-----LRSLTLLRALGAQKEAISPPDAASAAP-----LRTITADTERKLF	142		
DB 141	LIGGEDRVLKSCVYTLAAWGEQILFVGPAGSGHAKALNNVYSATGLLATIEALHVAQRF	200		
QY 143	RVYSNLFRLGKCLKLYTGEA 160			
DB 201	GIEPEVMTVLNTSTGRS 218			
RESULT 10				
Q9H2M7	PRELIMINARY; PRT; 339 AA.			
AC Q9H2M7				
DT 01-MAR-2001	(TrEMBLrel. 16, Created)			
DT 01-MAR-2002	(TrEMBLrel. 16, Last sequence update)			
DT 01-JUN-2002	(TrEMBLrel. 21, Last annotation update)			
DE UDP-N-acetylpyruvoylglucosamine reductase.				
GN MURB OR PA2977.				
OS Pseudomonas aeruginosa.				
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;				
OC Pseudomonas.				
OX NCBI_TaxID=287;				
ON [1]				
RP STRAIN=ATCC 15692 / PA01;				
RC MEDLINE=20437337; PubMed=10984043;				
RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,				
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,				
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,				
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,				
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,				
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;				
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an				
RT opportunistic pathogen."				
RL Nature 406:959-964 (2000).				
RM EMBL; AE004723; AAG06365.1; .				
DR HSSP; A08373; 2MBR.				
DR InterPro; IPR003170; MurB.				
DR InterPro; IPR001575; Oxid_FAD_bind.				
DR InterPro; IPR000531; TonB_boxC.				
DR Pfam; PF01565; FAD_binding_4; 1.				
DR Pfam; PF02873; MurB_C; 1.				
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.				
DR Complete proteome.				
QY SEQUENCE 339 AA; 37627 MW; C0C8EF9F2938FE27 CRC64;				
Query Match	9.8%	Score 83	DB 16	Length 339

Best Local Similarity 22.7%; Pred. No. 4.3;
Matches 41; Conservative 22; Mismatches 48; Indels 70; Gaps 8;

QY 31 EHCSLNE-NITVPDTRVNYAKRMEVGGQAVEVWQGLALLSEAVLRGQALLV-----82

Db 7 EHCSLKPYNTFGIDVRARLLAHARDE-----ADVREALALARE---RGLPLLVIGGNSL 58

QY 83 -----NSSQPWEP-LQLHVDKAVSGLSRLTITLL 109

Db 59 LLTRDVEALVLRNASOGRRIIVSDAADSVLVEAEAGEAWDPFVQWSLRLGLAGLNLILI- 117

QY 110 RALGAQKEAISPPDAASAAPLRTITA-----DTFRKLFRVYSNFRGLKLYTGEACRT 163

Db 118 -----PGTVGAAPMQNIGAYGVELKDVFDLTL--DRODGTREFDRQACRF 163

QY 164 G 164

Db 164 G 164

RESULT 11

Q9DHD6 PRELIMINARY; PRT; 3033 AA.

AC Q9DHD6; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70) (NS1)]

OS Hepatitis C virus type 2b.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=31650;

RN [1]

RC STRAIN=MA;

RX MEDLINE=21296595; PubMed=11402859;

RA Murakami K., Abe M., Kagayama T., Kamoshita N., Nomoto A.;

RT "Down-regulation of translation driven by hepatitis C virus internal

RL ribosomal entry site by the 3' untranslated region of RNA.;"

RL Arch. Virol. 146:729-741(2001).

CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.

DR EMBL; AB030907; HAV08107.1; -;

DR HSP; P27958; IAI.

DR InterPro; IPR000345; CytC_heme_bind.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR002522; HCV_capsid.

DR InterPro; IPR002521; HCV_core.

DR InterPro; IPR002519; HCV_env.

DR InterPro; IPR002531; HCV_NS1.

DR InterPro; IPR002518; HCV_NS2.

DR InterPro; IPR004109; HCV_NS3.

DR InterPro; IPR000745; HCV_NS4a.

DR InterPro; IPR001490; HCV_NS4b.

DR InterPro; IPR002868; HCV_NS5a.

DR InterPro; IPR002166; HCV_RdRp.

DR Pfam; PF01543; HCV_capsid; 1.

DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01539; HCV_env; 1.

DR Pfam; PF01560; HCV_NS1; 1.

DR Pfam; PF01538; HCV_NS2; 1.

DR Pfam; PF02907; HCV_NS3; 1.

DR Pfam; PF01006; HCV_NS4a; 1.

DR Pfam; PF01001; HCV_NS4b; 1.

DR Pfam; PF01506; HCV_NS5a; 1.

DR Pfam; PF00998; HCV_RdRp; 1.

DR ProDom; PD186062; HCV_NS1; 1.

DR SMART; SM00487; DEXDC; 1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; RNA-directed RNA polymerase; Transmembrane.

FT CHAIN 1 191 CORE PROTEIN.

FT CHAIN 192 383 E1 PROTEIN.

FT CHAIN 384 750 E2 PROTEIN.

FT CHAIN 751 813 P7 PROTEIN.

FT CHAIN 814 1030 NS2 PROTEIN.

FT CHAIN 1031 1561 NS3 PROTEINASE/HELICASE.

FT CHAIN 1562 1715 NS4A PROTEIN.

FT CHAIN 1716 1976 NS4B PROTEIN.

FT CHAIN 1977 2442 NS5A PROTEIN.

FT CHAIN 2443 3033 NS5B RNA-DEPENDENT RNA POLYMERASE.

SQ SEQUENCE 3033 AA; 329981 MW; 6B183PED090872B4 CRC64;

Query Match 9.8%; Score 82.5; DB 12; Length 3033;

Best Local Similarity 27.0%; Pred. No. 78;

Matches 40; Conservative 21; Mismatches 60; Indels 27; Gaps 7;

QY 11 VLRYLLLEAKAEENITTCGAE---HCSLNENITV-PDTKVNFYAKRM-----EV 56

Db 1665 VLAGGVLAAYCYLATGCSIIIGRIHLNDQVVVAPQKEILYEADEMECAKAAALIEE 1724

QY 57 GQAAVEVWQ--LALLSEAVLRGQALLVNSSQPWEPLQ-----LHVDKAVSGLSRLTLLR 110

Db 1725 GORMAEMLSKILGLLQATKQADIQAPMGSSWPKTEQFWARHWNFNISGIQYLAGLST 1784

QY 111 ALG-----AQEKAISPPDAASAAPLRTIT 134

Db 1785 LPGNPAVASMMAFS---AALTSPPLTST 1809

RESULT 12

Q9FK91 PRELIMINARY; PRT; 815 AA.

AC Q9FK91; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE Seed maturation protein PM38 protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RC SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RX MEDLINE=98403884; PubMed=9734815;

RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,

RA Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.

RT Sequence features of the regions of 1,367,185 bp covered by 19

RT Physically assigned P1 and TAC clones.;"

RL DNA Res. 5:203-216(1998).

DR EMBL; AB012244; BAB09119.1; -;

DR InterPro; IPR002086; Aldehyde_dehydr.

DR InterPro; IPR001357; BRCT.

DR InterPro; IPR001290; PARP.

DR Pfam; PF00533; BRCT; 1.

DR Pfam; PF00644; PARP; 1.

DR SMART; SM00292; BRCT; 1.

DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.

DR PROSITE; PS0172; BRCT; 1.

SQ SEQUENCE 815 AA; 91534 MW; 4B1B602057D46B60 CRC64;

Query Match 9.7%; Score 82; DB 10; Length 815;

Best Local Similarity 21.8%; Pred. No. 16;

Matches 42; Conservative 29; Mismatches 52; Indels 70; Gaps 12;

QY 21 EAENITTCGA-----EHCSLNENITVPTKVNFYAKRMEVG-----QQAQVEVW 64

Db 328 EKDGLLYNCAFSICDLGGRNEYC-IMQLVTVPDNSLAWY-FKRKGVGDDPNAERLSEW 385

QY 65 QGLALLSEAVLRGQALLV-----NSSQWE-----PLQ-----LHVDKAVSGL 102

Db 386 ED-----EAAIKFEARLFEELAGFEFWEKKEKTKPKHFFPDMDDGIEVRSGLGL 441

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Qy 103 RSL-----TTLLRALGAQ-----KEAISPDPDAASAPLRTITADTFKRL 141
Db 442 RQLGASAHCKLDSFVANEIKVLCGGEIYNVALMELGLDPPD-----LPMGMLTDIHLKRC 497
Qy 142 FRYNSFLRGKX 154
Db 498 EEVLLEFVE-KVK 509

RESULT 13
O86808 PRELIMINARY; PRT: 1829 AA.
AC O86808;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative sensory histidine kinase.
GN SCO5748 OR SC7C7.03.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Harris D., Taylor K.;
RA Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RA Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RA MEDLINE=97000351; PubMed=8843436;
RA "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
CC KINASES.
CC EMBL; AL031031; CAAL19849.1; -.
DR HSP; P52934; 1D23.
DR InterPro; IPR003594; AtPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00572; HAMP; 11.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00072; response_reg; 1.
DR Pfam; PF00512; signal; 1.
DR PRINTS; PR00344; BCTRLSENSOR.

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DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00304; HAMP; 12.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HSKA; 1.
DR SMART; SM00448; REC; 1.
KW Kinase; Phosphorylation; Sensory transduction; Transferase.
SQ SEQUENCE 1829 AA; 195751 MW; C9C8699938C956A4 CRC64;

Query Match 9.4%; Score 79.5; DB 16; Length 1829;
Best Local Similarity 22.8%; Pred. No. 82;
Matches 37; Conservative 29; Mismatches 61; Indels 35; Gaps 6;

Qy 18 EAKEENITTCGAHCSEINENITVPDTKVNFAWKRMVEGQAVVWQGLALL----- 70
Db 328 QVREISHVTTAVA-NGDLSKRVTVP-----ARGEVAQLAETINQMTELRIFADEV 377
Qy 71 -----SEAVLRGQALVNSSQWPEPLQHLHVDKAVSGLRSLTTLRLALGAOKEAISPP 122
Db 378 TRVANETGGEGQLGGQANVPCAACINKDL--TDSVNTVFNLTQVRDIAAVTTAVASG 434
Qy 123 DAASAAPLRTITADTFKRLFRVYS--NFLRGKCLKLYTGEACR 162
Db 435 DLS-----QKVTVDVAGEMLELXKNTVNTMTVDLSAFGAQEVTR 471

RESULT 14
Q91ZAI PRELIMINARY; PRT: 3033 AA.
AC Q91ZAI;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70)
DE (NSI)].
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MD2B-1;
RA Itakura J., Nagayama K., Enomoto N., Kurosaki M., Watanabe H.,
RA Sato C.;
RA "Full length cDNA sequence of HCV genotype 2b, strain MD2B-1.";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL; AF238486; AAF59945.1; -.
DR HSP; P27958; IHEI.
DR MEROPS; S29.001; -.
DR MEROPS; U39.001; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002522; HCV_capsid.
DR InterPro; IPR002521; HCV_core.
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR002531; HCV_NS1.
DR InterPro; IPR002518; HCV_NS2.
DR InterPro; IPR004109; HCV_NS3.
DR InterPro; IPR000745; HCV_NS4a.
DR InterPro; IPR001490; HCV_NS4b.
DR InterPro; IPR002868; HCV_NS5a.
DR InterPro; IPR002166; HCV_RdRp.
DR Pfam; PF01543; HCV_core; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Pfam; PF01538; HCV_NS2; 1.
DR Pfam; PF02907; HCV_NS3; 1.
DR Pfam; PF01006; HCV_NS4a; 1.
DR Pfam; PF01001; HCV_NS4b; 1.
DR Pfam; PF01506; HCV_NS5a; 1.
DR Pfam; PF00998; HCV_RdRp; 1.

```




STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

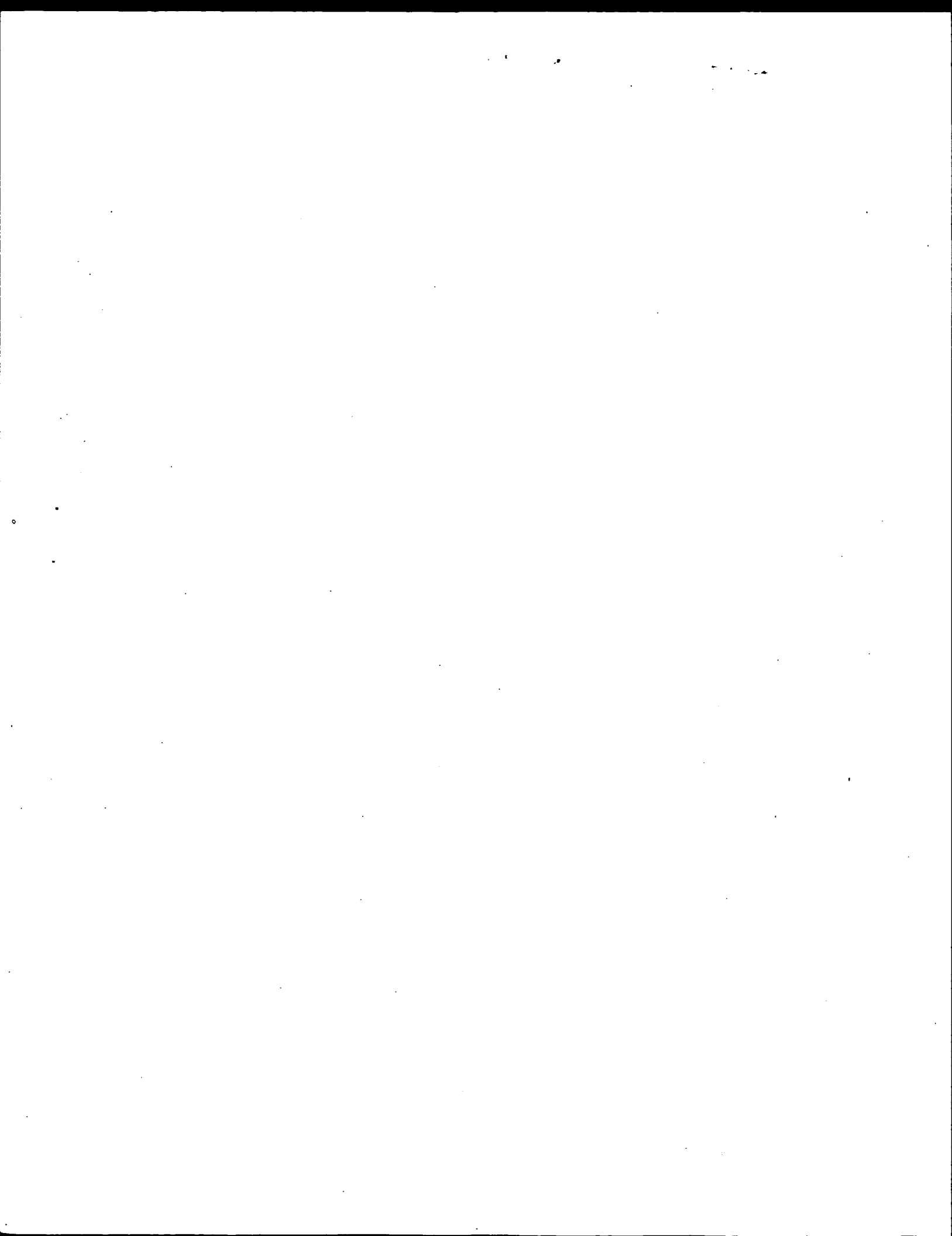
➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 – Circ. Desk







STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96531

TO: Patricia Patten
Location: cm1/11E09.
Art Unit: 1654
Friday, June 13, 2003

Case Serial Number: 830964

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Patten,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib

96531

From: Patten, Patricia
Sent: Friday, June 13, 2003 11:45 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search

Please search SEQ ID No. 1 of 09/830,964

Thank you.

Patricia Patten
1654 CM1 11E09
308-1189

Edward Hari
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 06/13/03
Date Completed: 06/13/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 02
WWW/Internet: _____
Other (specify): _____

